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(54) Title: HUMAN GENES DIFFERENTIALLY EXPRESSED IN COLORECTAL CANCER		
(57) Abstract This invention relates to novel human genes, to proteins expressed by the genes, and to variants of the proteins. The invention also relates to diagnostic assays and therapeutic agents related to the genes and proteins, including probes, antisense constructs, and antibodies. The subject nucleic acids have been found to be differentially regulated in tumor cells, particularly in colon cancer tissue.		

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prognosis for the patient is poor, even after surgical resection of the cancerous tissue. Early detection of colorectal cancer therefore is important in that detection may significantly reduce its morbidity.

Invasive diagnostic methods such as endoscopic examination allow for direct
5 visual identification, removal, and biopsy of potentially cancerous growths such as polyps. Endoscopy is expensive, uncomfortable, inherently risky, and therefore not a practical tool for screening populations to identify those with colorectal cancer. Non-invasive analysis of stool samples for characteristics indicative of the presence of colorectal cancer or precancer is a preferred alternative for early diagnosis, but no
10 known diagnostic method is available which reliably achieves this goal. A reliable, non-invasive, and accurate technique for diagnosing colon cancer at an early stage would help save many lives.

Summary of the Invention

15 The present invention provides nucleic acid sequences and proteins encoded thereby, as well as probes derived from the nucleic acid sequences, antibodies directed to the encoded proteins, and diagnostic methods for detecting cancerous cells, especially colon cancer cells. The sequences disclosed herein have been found to be
20 differentially expressed in samples obtained from colon cancer cell lines and/or colon cancer tissue. The 544 sequences that were obtained were analyzed by "blasting" the sequences against the publicly available databases; based upon the Blast search results it was found that SEQ ID Nos: 1-35 contained novel sequences, SEQ ID Nos: 36-168 contained EST sequences and SEQ ID Nos: 169-544 contained known sequences.

25 In one aspect, the invention provides an isolated nucleic acid comprising a nucleotide sequence which hybridizes under stringent conditions to a sequence of SEQ ID Nos. 1-544 or a sequence complementary thereto. In a related embodiment, the nucleic acid is at least about 80% or about 100% identical to a sequence corresponding to at least about 12, at least about 15, at least about 25, or at least about
30 40 consecutive nucleotides up to the full length of one of SEQ ID Nos. 1-544 or a sequence complementary thereto or up to the full length of the gene of which said sequence is a fragment. In certain embodiments, a nucleic acid of the present invention includes at least about five, at least about ten, or at least about twenty

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nucleic acids from a region designated as novel in Table 2. In certain other embodiments, a nucleic acid of the present invention includes at least about five, at least about ten, or at least about twenty nucleotides which are not included in corresponding clones whose accession numbers are listed in Table 2.

5 In another aspect, the invention provides an isolated nucleic acid comprising a nucleotide sequence which hybridizes under stringent conditions to a sequence of SEQ ID Nos. 1-168, preferably SEQ ID Nos. 1-35, or a sequence complementary thereto. In a related embodiment, the nucleic acid is at least about 80% or about 100% identical to a sequence corresponding to at least about 12, at least about 15, at
10 least about 25, or at least about 40 consecutive nucleotides up to the full length of one of SEQ ID Nos. 1-168, preferably SEQ ID Nos. 1-35 or a sequence complementary thereto or up to the full length of the gene of which said sequence is a fragment. In certain embodiments, a nucleic acid of the present invention includes at least about five, at least about ten, or at least about twenty nucleic acids from a region designated
15 as novel in Table 2. In certain other embodiments, a nucleic acid of the present invention includes at least about five, at least about ten, or at least about twenty nucleotides which are not included in corresponding clones whose accession numbers are listed in Table 2.

In one embodiment, the invention provides a nucleic acid comprising a
20 nucleotide sequence which hybridizes under stringent conditions to a sequence of SEQ ID Nos. 1-168, preferably SEQ ID Nos. 1-35, or a sequence complementary thereto, and a transcriptional regulatory sequence operably linked to the nucleotide sequence to render the nucleotide sequence suitable for use as an expression vector. In another embodiment, the nucleic acid may be included in an expression vector capable
25 of replicating in a prokaryotic or eukaryotic cell. In a related embodiment, the invention provides a host cell transfected with the expression vector.

In another embodiment, the invention provides a transgenic animal having a transgene of a nucleic acid comprising a nucleotide sequence which hybridizes under stringent conditions to a sequence of SEQ ID Nos. 1-168, preferably SEQ ID Nos 1-
30 35, or a sequence complementary thereto incorporated in cells thereof. The transgene modifies the level of expression of the nucleic acid, the stability of a mRNA transcript of the nucleic acid, or the activity of the encoded product of the nucleic acid.

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In yet another embodiment, the invention provides substantially pure nucleic acid which hybridizes under stringent conditions to a nucleic acid probe corresponding to at least about 12, at least about 15, at least about 25, or at least about 40 consecutive nucleotides up to the full length of one of SEQ ID Nos. 1-168, preferably SEQ ID Nos 1-35, or a sequence complementary thereto or up to the full length of the gene of which said sequence is a fragment. The invention also provides an antisense oligonucleotide analog which hybridizes under stringent conditions to at least 12, at least 25, or at least 50 consecutive nucleotides of one of SEQ ID Nos. 1-544 up to the full length of one of SEQ ID Nos. 1-544 or a sequence complementary thereto or up to the full length of the gene of which said sequence is a fragment, and which is resistant to cleavage by a nuclease, preferably an endogenous endonuclease or exonuclease.

In another embodiment, the invention provides a probe/primer comprising a substantially purified oligonucleotide, said oligonucleotide containing a region of nucleotide sequence which hybridizes under stringent conditions to at least about 12, at least about 15, at least about 25, or at least about 40 consecutive nucleotides of sense or antisense sequence selected from SEQ ID Nos. 1-168 up to the full length of one of SEQ ID Nos. 1-168 or a sequence complementary thereto or up to the full length of the gene of which said sequence is a fragment. In preferred embodiments, the probe selectively hybridizes with a target nucleic acid. In another embodiment, the probe may include a label group attached thereto and able to be detected. The label group may be selected from radioisotopes, fluorescent compounds, enzymes, and enzyme co-factors. The invention further provides arrays of at least about 10, at least about 25, at least about 50, or at least about 100 different probes as described above attached to a solid support.

In yet another embodiment, the invention pertains to a method of determining the phenotype of a cell, comprising detecting the differential expression, relative to a normal cell, of at least one nucleic acid which hybridizes under stringent conditions to one of SEQ ID Nos. 1-544, wherein the nucleic acid is differentially expressed by at least a factor of two, at least a factor of five, at least a factor of twenty, or at least a factor of fifty.

In another aspect, the invention provides polypeptides encoded by the subject nucleic acids. In one embodiment, the invention pertains to a polypeptide including an

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amino acid sequence encoded by a nucleic acid comprising a nucleotide sequence which hybridizes under stringent conditions to a sequence of SEQ ID Nos. 1-168 or a sequence complementary thereto, or a fragment comprising at least about 25, or at least about 40 amino acids thereof. Further provided are antibodies immunoreactive
5 with these polypeptides.

In still another aspect, the invention provides diagnostic methods. In one embodiment, the invention pertains to a method for determining the phenotype of cells from a patient by providing a nucleic acid probe comprising a nucleotide sequence having at least 12, at least about 15, at least about 25, or at least about 40
10 consecutive nucleotides represented in a sequence of SEQ ID Nos. 1-544 up to the full length of one of SEQ ID Nos. 1-544 or a sequence complementary thereto or up to the full length of the gene of which said sequence is a fragment, obtaining a sample of cells from a patient, providing a second sample of cells substantially all of which are non-cancerous, contacting the nucleic acid probe under stringent conditions with
15 mRNA of each of said first and second cell samples, and comparing (a) the amount of hybridization of the probe with mRNA of the first cell sample, with (b) the amount of hybridization of the probe with mRNA of the second cell sample, wherein a difference of at least a factor of two, at least a factor of five, at least a factor of twenty, or at least a factor of fifty in the amount of hybridization with the mRNA of the first cell sample
20 as compared to the amount of hybridization with the mRNA of the second cell sample is indicative of the phenotype of cells in the first cell sample. Determining the phenotype includes determining the genotype, as the term is used herein.

In another embodiment, the invention provides a test kit for identifying an transformed cells, comprising a probe/primer as described above, for measuring a
25 level of a nucleic acid which hybridizes under stringent conditions to a nucleic acid of SEQ ID Nos. 1-544 in a sample of cells isolated from a patient. In certain embodiments, the kit may further include instructions for using the kit, solutions for suspending or fixing the cells, detectable tags or labels, solutions for rendering a nucleic acid susceptible to hybridization, solutions for lysing cells, or solutions for the
30 purification of nucleic acids.

In another embodiment, the invention provides a method of determining the phenotype of a cell, comprising detecting the differential expression, relative to a normal cell, of at least one protein encoded by a nucleic acid which hybridizes under

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stringent conditions to one of SEQ ID Nos. 1-544, wherein the protein is differentially expressed by at least a factor of two, at least a factor of five, at least a factor of twenty, or at least a factor of fifty. In one embodiment, the level of the protein is detected in an immunoassay. The invention also pertains to a method for determining the

5 presence or absence of a nucleic acid which hybridizes under stringent conditions to one of SEQ ID Nos. 1-168 in a cell, comprising contacting the cell with a probe as described above. The invention further provides a method for determining the presence or absence of a subject polypeptide encoded by a nucleic acid which hybridizes under stringent conditions to one of SEQ ID Nos. 1-168 in a cell,

10 comprising contacting the cell with an antibody as described above. In yet another embodiment, the invention provides a method for determining the presence of an aberrant mutation (e.g., deletion insertion, or substitution of nucleic acids) or aberrant methylation in a gene which hybridizes under stringent conditions to a sequence of SEQ ID Nos. 1-168 or a sequence complementary thereto, comprising collecting a

15 sample of cells from a patient, isolating nucleic acid from the cells of the sample, contacting the nucleic acid sample with one or more primers which specifically hybridize to a nucleic acid sequence of SEQ ID Nos. 1-544 under conditions such that hybridization and amplification of the nucleic acid occurs, and comparing the presence, absence, or size of an amplification product to the amplification product of a

20 normal cell.

In one embodiment, the invention provides a test kit for identifying transformed cells, comprising an antibody specific for a protein encoded by a nucleic acid which hybridizes under stringent conditions to any one of SEQ Nos. 1-544. In certain embodiments, the kit further includes instructions for using the kit. In certain

25 embodiments, the kit may further include instructions for using the kit, solutions for suspending or fixing the cells, detectable tags or labels, solutions for rendering a polypeptide susceptible to the binding of an antibody, solutions for lysing cells, or solutions for the purification of polypeptides.

In yet another aspect, the invention provides pharmaceutical compositions

30 including the subject nucleic acids. In one embodiment, an agent which alters the level of expression in a cell of a nucleic acid which hybridizes under stringent conditions to one of SEQ ID Nos. 1-544 or a sequence complementary thereto is identified by providing a cell, treating the cell with a test agent, determining the level

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of expression in the cell of a nucleic acid which hybridizes under stringent conditions to one of SEQ ID Nos. 1-544 or a sequence complementary thereto, and comparing the level of expression of the nucleic acid in the treated cell with the level of expression of the nucleic acid in an untreated cell, wherein a change in the level of expression of the nucleic acid in the treated cell relative to the level of expression of the nucleic acid in the untreated cell is indicative of an agent which alters the level of expression of the nucleic acid in a cell. The invention further provides a pharmaceutical composition comprising an agent identified by this method. In another embodiment, the invention provides a pharmaceutical composition which includes a polypeptide encoded by a nucleic acid having a nucleotide sequence that hybridizes under stringent conditions to one of SEQ ID Nos. 1-544 or a sequence complementary thereto. In one embodiment, the invention pertains to a pharmaceutical composition comprising a nucleic acid including a sequence which hybridizes under stringent conditions to one of SEQ ID Nos. 1-544 or a sequence complementary thereto.

Brief Description of the Figure

The figure depicts an exemplary assay result for determining differential expression of gene products in cells.

Detailed Description of the Invention

The invention relates to nucleic acids having the disclosed nucleotide sequences (SEQ ID Nos. 1-544), as well as full length cDNA, mRNA, and genes corresponding to these sequences, and to polypeptides and proteins encoded by these nucleic acids and genes, and portions thereof.

Also included are polypeptides and proteins encoded by the nucleic acids of SEQ ID Nos. 1-544. The various nucleic acids that can encode these polypeptides and proteins differ because of the degeneracy of the genetic code, in that most amino acids are encoded by more than one triplet codon. The identity of such codons is well known in this art, and this information can be used for the construction of the nucleic acids within the scope of the invention.

Nucleic acids encoding polypeptides and proteins that are variants of the polypeptides and proteins encoded by the nucleic acids and related cDNA and genes are also within the scope of the invention. The variants differ from wild-type protein in having one or more amino acid substitutions that either enhance, add, or diminish a

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biological activity of the wild-type protein. Once the amino acid change is selected, a nucleic acid encoding that variant is constructed according to the invention.

The following detailed description discloses how to obtain or make full-length cDNA and human genes corresponding to the nucleic acids, how to express these
5 nucleic acids and genes, how to identify structural motifs of the genes, how to identify the function of a protein encoded by a gene corresponding to an nucleic acid, how to use nucleic acids as probes in mapping and in tissue profiling, how to use the corresponding polypeptides and proteins to raise antibodies, and how to use the nucleic acids, polypeptides, and proteins for therapeutic and diagnostic purposes.

10 The sequences investigated herein have been found to be differentially expressed in samples obtained from colon cancer tissue. However, it is also believed that these sequences may also have utility with other types of cancer. In a related application, PCT/IB99/01062, filed June 9, 1999, the inventors disclosed nucleic acid sequences that are differentially expressed in colon cancer-derived cell lines, such as
15 SW 480, relative to the expression levels in normal tissue, e.g., normal colon tissue and/or normal non-colon tissue. In this application, Table 3 lists nucleic acid sequences which are over-expressed in both cancer cell line SW 480 as well colon cancer tissue obtained from various patients.

Accordingly, certain aspects of the present invention relate to nucleic acids
20 differentially expressed in tumor tissue, especially colon cancer cell lines, polypeptides encoded by such nucleic acids, and antibodies immunoreactive with these polypeptides, and preparations of such compositions. Moreover, the present invention provides diagnostic and therapeutic assays and reagents for detecting and treating disorders involving, for example, aberrant expression of the subject nucleic
25 acids.

I. General

This invention relates in part to novel methods for identifying and/or classifying cancerous cells present in a human tumors, particularly in solid tumors,
30 e.g., carcinomas and sarcomas, such as, for example, breast or colon cancers. The method uses genes that are differentially expressed in cancer cell lines and/or cancer tissue compared with related normal cells, such as normal colon cells, and thereby

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identifies or classifies tumor cells by the upregulation and/or downregulation of expression of particular genes, an event which is implicated in tumorigenesis.

Upregulation or increased expression of certain genes such as oncogenes, act to promote malignant growth. Downregulation or decreased expression of genes such as tumor suppressor genes also promotes malignant growth. Thus, alteration in the expression of either type of gene is a potential diagnostic indicator for determining whether a subject is at risk of developing or has cancer, e.g., colon cancer.

Accordingly, in one aspect, the invention also provides biomarkers, such as nucleic acid markers, for human tumor cells, e.g., for colon cancer cells. The invention also provides proteins encoded by these nucleic acid markers.

The invention also features methods for identifying drugs useful for treatment of such cancer cells, and for treatment of a cancerous condition, such as colon cancer. Unlike prior methods, the invention provides a means for identifying cancer cells at an early stage of development, so that premalignant cells can be identified prior to their spreading throughout the human body. This allows early detection of potentially cancerous conditions, and treatment of those cancerous conditions prior to spread of the cancerous cells throughout the body, or prior to development of an irreversible cancerous condition.

II. Definitions

For convenience, the meaning of certain terms and phrases used in the specification, examples, and appended claims, are provided below.

The term "an aberrant expression", as applied to a nucleic acid of the present invention, refers to level of expression of that nucleic acid which differs from the level of expression of that nucleic acid in healthy tissue, or which differs from the activity of the polypeptide present in a healthy subject. An activity of a polypeptide can be aberrant because it is stronger than the activity of its native counterpart. Alternatively, an activity can be aberrant because it is weaker or absent relative to the activity of its native counterpart. An aberrant activity can also be a change in the activity; for example, an aberrant polypeptide can interact with a different target peptide. A cell can have an aberrant expression level of a gene due to overexpression or underexpression of that gene.

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The term "agonist", as used herein, is meant to refer to an agent that mimics or upregulates (e.g., potentiates or supplements) the bioactivity of a protein. An agonist can be a wild-type protein or derivative thereof having at least one bioactivity of the wild-type protein. An agonist can also be a compound that upregulates expression of a gene or which increases at least one bioactivity of a protein. An agonist can also be a compound which increases the interaction of a polypeptide with another molecule, e.g., a target peptide or nucleic acid.

The term "allele", which is used interchangeably herein with "allelic variant", refers to alternative forms of a gene or portions thereof. Alleles occupy the same locus or position on homologous chromosomes. When a subject has two identical alleles of a gene, the subject is said to be homozygous for that gene or allele. When a subject has two different alleles of a gene, the subject is said to be heterozygous for the gene. Alleles of a specific gene can differ from each other in a single nucleotide, or several nucleotides, and can include substitutions, deletions, and/or insertions of nucleotides. An allele of a gene can also be a form of a gene containing mutations.

The term "allelic variant of a polymorphic region of a gene" refers to a region of a gene having one of several nucleotide sequences found in that region of the gene in other individuals.

"Antagonist" as used herein is meant to refer to an agent that downregulates (e.g., suppresses or inhibits) at least one bioactivity of a protein. An antagonist can be a compound which inhibits or decreases the interaction between a protein and another molecule, e.g., a target peptide or enzyme substrate. An antagonist can also be a compound that downregulates expression of a gene or which reduces the amount of expressed protein present.

The term "antibody" as used herein is intended to include whole antibodies, e.g., of any isotype (IgG, IgA, IgM, IgE, etc), and includes fragments thereof which are also specifically reactive with a vertebrate, e.g., mammalian, protein. Antibodies can be fragmented using conventional techniques and the fragments screened for utility in the same manner as described above for whole antibodies. Thus, the term includes segments of proteolytically-cleaved or recombinantly-prepared portions of an antibody molecule that are capable of selectively reacting with a certain protein. Nonlimiting examples of such proteolytic and/or recombinant fragments include Fab, F(ab')₂, Fab', Fv, and single chain antibodies (scFv) containing a V[L] and/or V[H]

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domain joined by a peptide linker. The scFv's may be covalently or non-covalently linked to form antibodies having two or more binding sites. The subject invention includes polyclonal, monoclonal, or other purified preparations of antibodies and recombinant antibodies.

5 The phenomenon of "apoptosis" is well known, and can be described as a programmed death of cells. As is known, apoptosis is contrasted with "necrosis", a phenomenon when cells die as a result of being killed by a toxic material, or other external effect. Apoptosis involves chromatic condensation, membrane blebbing, and fragmentation of DNA, all of which are generally visible upon microscopic
10 examination.

A disease, disorder, or condition "associated with" or "characterized by" an aberrant expression of a nucleic acid refers to a disease, disorder, or condition in a subject which is caused by, contributed to by, or causative of an aberrant level of expression of a nucleic acid.

15 As used herein the term "bioactive fragment of a polypeptide" refers to a fragment of a full-length polypeptide, wherein the fragment specifically agonizes (mimics) or antagonizes (inhibits) the activity of a wild-type polypeptide. The bioactive fragment preferably is a fragment capable of interacting with at least one other molecule, e.g., protein, small molecule, or DNA, which a full length protein can
20 bind.

"Biological activity" or "bioactivity" or "activity" or "biological function", which are used interchangeably, herein mean an effector or antigenic function that is directly or indirectly performed by a polypeptide (whether in its native or denatured conformation), or by any subsequence thereof. Biological activities include binding
25 to polypeptides, binding to other proteins or molecules, activity as a DNA binding protein, as a transcription regulator, ability to bind damaged DNA, etc. A bioactivity can be modulated by directly affecting the subject polypeptide. Alternatively, a bioactivity can be altered by modulating the level of the polypeptide, such as by modulating expression of the corresponding gene.

30 The term "biomarker" refers a biological molecule, e.g., a nucleic acid, peptide, hormone, etc., whose presence or concentration can be detected and correlated with a known condition, such as a disease state.

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"Cells," "host cells", or "recombinant host cells" are terms used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A "chimeric polypeptide" or "fusion polypeptide" is a fusion of a first amino acid sequence encoding one of the subject polypeptides with a second amino acid sequence defining a domain (e.g., polypeptide portion) foreign to and not substantially homologous with any domain of the subject polypeptide. A chimeric polypeptide may present a foreign domain which is found (albeit in a different polypeptide) in an organism which also expresses the first polypeptide, or it may be an "interspecies," "intergenic," etc., fusion of polypeptide structures expressed by different kinds of organisms. In general, a fusion polypeptide can be represented by the general formula $(X)_n-(Y)_m-(Z)_n$, wherein Y represents a portion of the subject polypeptide, and X and Z are each independently absent or represent amino acid sequences which are not related to the native sequence found in an organism, or which are not found as a polypeptide chain contiguous with the subject sequence, where m is an integer greater than or equal to one, and each occurrence of n is, independently, 0 or an integer greater than or equal to 1 (n and m are preferably no greater than 5 or 10).

A "delivery complex" shall mean a targeting means (e.g., a molecule that results in higher affinity binding of a nucleic acid, protein, polypeptide or peptide to a target cell surface and/or increased cellular or nuclear uptake by a target cell). Examples of targeting means include: sterols (e.g., cholesterol), lipids (e.g., a cationic lipid, virosome or liposome), viruses (e.g., adenovirus, adeno-associated virus, and retrovirus), or target cell-specific binding agents (e.g., ligands recognized by target cell specific receptors). Preferred complexes are sufficiently stable *in vivo* to prevent significant uncoupling prior to internalization by the target cell. However, the complex is cleavable under appropriate conditions within the cell so that the nucleic acid, protein, polypeptide or peptide is released in a functional form.

As is well known, genes or a particular polypeptide may exist in single or multiple copies within the genome of an individual. Such duplicate genes may be identical or may have certain modifications, including nucleotide substitutions,

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additions or deletions, which all still code for polypeptides having substantially the same activity. The term "DNA sequence encoding a polypeptide" may thus refer to one or more genes within a particular individual. Moreover, certain differences in nucleotide sequences may exist between individual organisms, which are called
5 alleles. Such allelic differences may or may not result in differences in amino acid sequence of the encoded polypeptide yet still encode a polypeptide with the same biological activity.

The term "equivalent" is understood to include nucleotide sequences encoding functionally equivalent polypeptides. Equivalent nucleotide sequences will include
10 sequences that differ by one or more nucleotide substitutions, additions or deletions, such as allelic variants; and will, therefore, include sequences that differ from the nucleotide sequence of the nucleic acids shown in SEQ ID NOs: 1-544 due to the degeneracy of the genetic code.

As used herein, the terms "gene", "recombinant gene", and "gene construct"
15 refer to a nucleic acid of the present invention associated with an open reading frame, including both exon and (optionally) intron sequences.

A "recombinant gene" refers to nucleic acid encoding a polypeptide and comprising exon sequences, though it may optionally include intron sequences which are derived from, for example, a related or unrelated chromosomal gene. The term
20 "intron" refers to a DNA sequence present in a given gene which is not translated into protein and is generally found between exons.

The term "growth" or "growth state" of a cell refers to the proliferative state of a cell as well as to its differentiative state. Accordingly, the term refers to the phase of the cell cycle in which the cell is, e.g., G0, G1, G2, prophase, metaphase, or telophase,
25 as well as to its state of differentiation, e.g., undifferentiated, partially differentiated, or fully differentiated. Without wanting to be limited, differentiation of a cell is usually accompanied by a decrease in the proliferative rate of a cell.

"Homology" or "identity" or "similarity" refers to sequence similarity between two peptides or between two nucleic acid molecules, with identity being a more strict
30 comparison. Homology and identity can each be determined by comparing a position in each sequence which may be aligned for purposes of comparison. When a position in the compared sequence is occupied by the same base or amino acid, then the molecules are identical at that position. A degree of homology or similarity or

identity between nucleic acid sequences is a function of the number of identical or matching nucleotides at positions shared by the nucleic acid sequences. A degree of identity of amino acid sequences is a function of the number of identical amino acids at positions shared by the amino acid sequences. A degree of homology or similarity of amino acid sequences is a function of the number of amino acids, i.e., structurally related, at positions shared by the amino acid sequences. An "unrelated" or "non-homologous" sequence shares less than 40% identity, though preferably less than 25% identity, with one of the sequences of the present invention.

The term "percent identical" refers to sequence identity between two amino acid sequences or between two nucleotide sequences. Identity can each be determined by comparing a position in each sequence which may be aligned for purposes of comparison. When an equivalent position in the compared sequences is occupied by the same base or amino acid, then the molecules are identical at that position; when the equivalent site occupied by the same or a similar amino acid residue (e.g., similar in steric and/or electronic nature), then the molecules can be referred to as homologous (similar) at that position. Expression as a percentage of homology, similarity, or identity refers to a function of the number of identical or similar amino acids at positions shared by the compared sequences. Various alignment algorithms and/or programs may be used, including FASTA, BLAST, or ENTREZ. FASTA and BLAST are available as a part of the GCG sequence analysis package (University of Wisconsin, Madison, Wis.), and can be used with, e.g., default settings. ENTREZ is available through the National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health, Bethesda, Md. In one embodiment, the percent identity of two sequences can be determined by the GCG program with a gap weight of 1, e.g., each amino acid gap is weighted as if it were a single amino acid or nucleotide mismatch between the two sequences.

Other techniques for alignment are described in Methods in Enzymology, vol. 266: Computer Methods for Macromolecular Sequence Analysis (1996), ed. Doolittle, Academic Press, Inc., a division of Harcourt Brace & Co., San Diego, California, USA. Preferably, an alignment program that permits gaps in the sequence is utilized to align the sequences. The Smith-Waterman is one type of algorithm that permits gaps in sequence alignments. See Meth. Mol. Biol. 70: 173-187 (1997). Also, the GAP program using the Needleman and Wunsch alignment method can be utilized to

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align sequences. An alternative search strategy uses MPSRCH software, which runs on a MASPAR computer. MPSRCH uses a Smith-Waterman algorithm to score sequences on a massively parallel computer. This approach improves ability to pick up distantly related matches, and is especially tolerant of small gaps and nucleotide sequence errors. Nucleic acid-encoded amino acid sequences can be used to search both protein and DNA databases.

Databases with individual sequences are described in Methods in Enzymology, ed. Doolittle, *supra*. Databases include Genbank, EMBL, and DNA Database of Japan (DDBJ).

Preferred nucleic acids have a sequence at least 70%, and more preferably 80% identical and more preferably 90% and even more preferably at least 95% identical to a nucleic acid sequence of a sequence shown in one of SEQ ID NOS: 1-544. Nucleic acids at least 90%, more preferably 95%, and most preferably at least about 98-99% identical with a nucleic sequence represented in one of SEQ ID NOS: 1-544 are of course also within the scope of the invention. In preferred embodiments, the nucleic acid is mammalian.

The term "interact" as used herein is meant to include detectable interactions (e.g., biochemical interactions) between molecules, such as interaction between protein-protein, protein-nucleic acid, nucleic acid-nucleic acid, and protein-small molecule or nucleic acid-small molecule in nature.

The term "isolated" as used herein with respect to nucleic acids, such as DNA or RNA, refers to molecules separated from other DNAs, or RNAs, respectively, that are present in the natural source of the macromolecule. The term isolated as used herein also refers to a nucleic acid or peptide that is substantially free of cellular material, viral material, or culture medium when produced by recombinant DNA techniques, or chemical precursors or other chemicals when chemically synthesized. Moreover, an "isolated nucleic acid" is meant to include nucleic acid fragments which are not naturally occurring as fragments and would not be found in the natural state. The term "isolated" is also used herein to refer to polypeptides which are isolated from other cellular proteins and is meant to encompass both purified and recombinant polypeptides.

The terms "modulated" and "differentially regulated" as used herein refer to both upregulation (i.e., activation or stimulation (e.g., by agonizing or potentiating))

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and downregulation (i.e., inhibition or suppression (e.g., by antagonizing, decreasing or inhibiting)).

The term "mutated gene" refers to an allelic form of a gene, which is capable of altering the phenotype of a subject having the mutated gene relative to a subject which does not have the mutated gene. If a subject must be homozygous for this mutation to have an altered phenotype, the mutation is said to be recessive. If one copy of the mutated gene is sufficient to alter the genotype of the subject, the mutation is said to be dominant. If a subject has one copy of the mutated gene and has a phenotype that is intermediate between that of a homozygous and that of a heterozygous subject (for that gene), the mutation is said to be co-dominant.

The designation "N", where it appears in the accompanying Sequence Listing, indicates that the identity of the corresponding nucleotide is unknown. "N" should therefore not necessarily be interpreted as permitting substitution with any nucleotide, e.g., A, T, C, or G, but rather as holding the place of a nucleotide whose identity has not been conclusively determined.

The "non-human animals" of the invention include mammals such as rodents, non-human primates, sheep, dog, cow, chickens, amphibians, reptiles, etc. Preferred non-human animals are selected from the rodent family including rat and mouse, most preferably mouse, though transgenic amphibians, such as members of the *Xenopus* genus, and transgenic chickens can also provide important tools for understanding and identifying agents which can affect, for example, embryogenesis and tissue formation. The term "chimeric animal" is used herein to refer to animals in which the recombinant gene is found, or in which the recombinant gene is expressed in some but not all cells of the animal. The term "tissue-specific chimeric animal" indicates that one of the recombinant genes is present and/or expressed or disrupted in some tissues but not others.

As used herein, the term "nucleic acid" refers to polynucleotides such as deoxyribonucleic acid (DNA), and, where appropriate, ribonucleic acid (RNA). The term should also be understood to include, as equivalents, analogs of either RNA or DNA made from nucleotide analogs, and, as applicable to the embodiment being described, single (sense or antisense) and double-stranded polynucleotides. ESTs, chromosomes, cDNAs, mRNAs, and rRNAs are representative examples of molecules that may be referred to as nucleic acids.

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The term "nucleotide sequence complementary to the nucleotide sequence of SEQ ID NO. x" refers to the nucleotide sequence of the complementary strand of a nucleic acid strand having SEQ ID NO. x. The term "complementary strand" is used herein interchangeably with the term "complement". The complement of a nucleic acid strand can be the complement of a coding strand or the complement of a non-coding strand.

The term "polymorphism" refers to the coexistence of more than one form of a gene or portion (e.g., allelic variant) thereof. A portion of a gene of which there are at least two different forms, i.e., two different nucleotide sequences, is referred to as a "polymorphic region of a gene". A polymorphic region can be a single nucleotide, the identity of which differs in different alleles. A polymorphic region can also be several nucleotides long.

A "polymorphic gene" refers to a gene having at least one polymorphic region.

As used herein, the term "promoter" means a DNA sequence that regulates expression of a selected DNA sequence operably linked to the promoter, and which effects expression of the selected DNA sequence in cells. The term encompasses "tissue specific" promoters, i.e., promoters which effect expression of the selected DNA sequence only in specific cells (e.g., cells of a specific tissue). The term also covers so-called "leaky" promoters, which regulate expression of a selected DNA primarily in one tissue, but cause expression in other tissues as well. The term also encompasses non-tissue specific promoters and promoters that constitutively expressed or that are inducible (i.e., expression levels can be controlled).

The terms "protein", "polypeptide", and "peptide" are used interchangeably herein when referring to a gene product.

The term "recombinant protein" refers to a polypeptide of the present invention which is produced by recombinant DNA techniques, wherein generally, DNA encoding a polypeptide is inserted into a suitable expression vector which is in turn used to transform a host cell to produce the heterologous protein. Moreover, the phrase "derived from", with respect to a recombinant gene, is meant to include within the meaning of "recombinant protein" those proteins having an amino acid sequence of a native polypeptide, or an amino acid sequence similar thereto which is generated by mutations including substitutions and deletions (including truncation) of a naturally occurring form of the polypeptide.

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"Small molecule" as used herein, is meant to refer to a composition, which has a molecular weight of less than about 5 kD and most preferably less than about 4 kD. Small molecules can be nucleic acids, peptides, polypeptides, peptidomimetics, carbohydrates, lipids or other organic (carbon-containing) or inorganic molecules.

5 Many pharmaceutical companies have extensive libraries of chemical and/or biological mixtures, often fungal, bacterial, or algal extracts, which can be screened with any of the assays of the invention to identify compounds that modulate a bioactivity.

As used herein, the term "specifically hybridizes" or "specifically detects" refers to the ability of a nucleic acid molecule of the invention to hybridize to at least a portion of, for example, approximately 6, 12, 15, 20, 30, 50, 100, 150, 200, 300, 350, 400, 500, 750, or 1000 contiguous nucleotides of a nucleic acid designated in any one of SEQ ID Nos: 1-544, or a sequence complementary thereto, or naturally occurring mutants thereof, such that it has less than 15%, preferably less than 10%, and more preferably less than 5% background hybridization to a cellular nucleic acid (e.g., mRNA or genomic DNA) encoding a different protein. In preferred
15 embodiments, the oligonucleotide probe detects only a specific nucleic acid, e.g., it does not substantially hybridize to similar or related nucleic acids, or complements thereof.

20 "Transcriptional regulatory sequence" is a generic term used throughout the specification to refer to DNA sequences, such as initiation signals, enhancers, and promoters, which induce or control transcription of protein coding sequences with which they are operably linked. In preferred embodiments, transcription of one of the genes is under the control of a promoter sequence (or other transcriptional regulatory sequence) which controls the expression of the recombinant gene in a cell-type in
25 which expression is intended. It will also be understood that the recombinant gene can be under the control of transcriptional regulatory sequences which are the same or which are different from those sequences which control transcription of the naturally-occurring forms of the polypeptide.

30 As used herein, the term "transfection" means the introduction of a nucleic acid, e.g., via an expression vector, into a recipient cell by nucleic acid-mediated gene transfer. "Transformation", as used herein, refers to a process in which a cell's genotype is changed as a result of the cellular uptake of exogenous DNA or RNA,

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and, for example, the transformed cell expresses a recombinant form of a polypeptide or, in the case of anti-sense expression from the transferred gene, the expression of the target gene is disrupted.

As used herein, the term "transgene" means a nucleic acid sequence (or an antisense transcript thereto) which has been introduced into a cell. A transgene could be partly or entirely heterologous, i.e., foreign, to the transgenic animal or cell into which it is introduced, or, is homologous to an endogenous gene of the transgenic animal or cell into which it is introduced, but which is designed to be inserted, or is inserted, into the animal's genome in such a way as to alter the genome of the cell into which it is inserted (e.g., it is inserted at a location which differs from that of the natural gene or its insertion results in a knockout). A transgene can also be present in a cell in the form of an episome. A transgene can include one or more transcriptional regulatory sequences and any other nucleic acid, such as introns, that may be necessary for optimal expression of a selected nucleic acid.

A "transgenic animal" refers to any animal, preferably a non-human mammal, bird or an amphibian, in which one or more of the cells of the animal contain heterologous nucleic acid introduced by way of human intervention, such as by transgenic techniques well known in the art. The nucleic acid is introduced into the cell, directly or indirectly by introduction into a precursor of the cell, by way of deliberate genetic manipulation, such as by microinjection or by infection with a recombinant virus. The term genetic manipulation does not include classical cross-breeding, or *in vitro* fertilization, but rather is directed to the introduction of a recombinant DNA molecule. This molecule may be integrated within a chromosome, or it may be extra-chromosomally replicating DNA. In the typical transgenic animals described herein, the transgene causes cells to express a recombinant form of one of the subject polypeptide, e.g. either agonistic or antagonistic forms. However, transgenic animals in which the recombinant gene is silent are also contemplated, as for example, the FLP or CRE recombinase dependent constructs described below. Moreover, "transgenic animal" also includes those recombinant animals in which gene disruption of one or more genes is caused by human intervention, including both recombination and antisense techniques.

The term "treating" as used herein is intended to encompass curing as well as ameliorating at least one symptom of the condition or disease.

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The term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of preferred vector is an episome, i.e., a nucleic acid capable of extra-chromosomal replication. Preferred vectors are those capable of autonomous replication and/or expression of nucleic acids to which they are linked. Vectors capable of directing the expression of genes to which they are operatively linked are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of "plasmids" which refer generally to circular double stranded DNA loops which, in their vector form are not bound to the chromosome. In the present specification, "plasmid" and "vector" are used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors which serve equivalent functions and which become known in the art subsequently hereto.

The term "wild-type allele" refers to an allele of a gene which, when present in two copies in a subject results in a wild-type phenotype. There can be several different wild-type alleles of a specific gene, since certain nucleotide changes in a gene may not affect the phenotype of a subject having two copies of the gene with the nucleotide changes.

III. Nucleic Acids of the Present Invention

As described below, one aspect of the invention pertains to isolated nucleic acids, variants, and/or equivalents of such nucleic acids.

Nucleic acids of the present invention have been identified as differentially expressed in tumor cells, e.g., colon cancer-derived cell lines (relative to the expression levels in normal tissue, e.g., normal colon tissue and/or normal non-colon tissue), such as SFO ID Nos. 1-544, preferably SEQ ID Nos. 1-168, even more preferably SEQ ID Nos. 1-35, or a sequence complementary thereto. In certain embodiments, the subject nucleic acids are differentially expressed by at least a factor of two, preferably at least a factor of five, even more preferably at least a factor of twenty, still more preferably at least a factor of fifty. Preferred nucleic acids include sequences identified as differentially expressed both in colon cancer cell tissue and colon cancer cell lines. In preferred embodiments, nucleic acids of the present invention are upregulated in tumor cells, especially colon cancer tissue and/or colon

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cancer-derived cell lines. In another embodiment, nucleic acids of the present invention are downregulated in tumor cells, especially colon cancer tissue and/or colon cancer-derived cell lines.

Table 1 indicates those sequences which are over- or underexpressed in a colon cancer-derived cell line relative to normal tissue, and further designates those sequences which are also differentially regulated in colon cancer tissue. The designation O indicates that the corresponding sequence was overexpressed, M indicates possible overexpression, N indicates no differential expression, and U indicates underexpression.

Genes which are upregulated, such as oncogenes, or downregulated, such as tumor suppressors, in aberrantly proliferating cells may be targets for diagnostic or therapeutic techniques. For example, upregulation of the *cdc2* gene induces mitosis. Overexpression of the *myt1* gene, a mitotic deactivator, negatively regulates the activity of *cdc2*. Aberrant proliferation may thus be induced either by upregulating *cdc2* or by downregulating *myt1*. Similarly, downregulation of tumor suppressors such as *p53* and *Rb* have been implicated in tumorigenesis.

Particularly preferred polypeptides are those that are encoded by nucleic acid sequences at least about 70%, 75%, 80%, 90%, 95%, 97%, or 98% similar to a nucleic acid sequence of SEQ ID Nos. 1-544. Preferably, the nucleic acid includes all or a portion (e.g., at least about 12, at least about 15, at least about 25, or at least about 40 nucleotides) of the nucleotide sequence corresponding to the nucleic acid of SEQ ID Nos. 1-168, preferably SEQ ID Nos. 1-35, or a sequence complementary thereto.

Still other preferred nucleic acids of the present invention encode a polypeptide comprising at least a portion of a polypeptide encoded by one of SEQ ID Nos. 1-544. For example, preferred nucleic acid molecules for use as probes/primers or antisense molecules (i.e., noncoding nucleic acid molecules) can comprise at least about 12, 20, 30, 50, 60, 70, 80, 90, or 100 base pairs in length up to the length of the complete gene. Coding nucleic acid molecules can comprise, for example, from about 50, 60, 70, 80, 90, or 100 base pairs up to the length of the complete gene.

Another aspect of the invention provides a nucleic acid which hybridizes under low, medium, or high stringency conditions to a nucleic acid sequence represented by one of SEQ ID Nos. 1-168, preferably SEQ ID Nos. 1-35, or a sequence complementary thereto. Appropriate stringency conditions which promote

DNA hybridization, for example, 6.0 x sodium chloride/sodium citrate (SSC) at about 45 °C, followed by a wash of 2.0 x SSC at 50 °C, are known to those skilled in the art or can be found in Current Protocols in Molecular Biology, John Wiley & Sons, N.Y. (1989), 6.3.1-12.3.6. For example, the salt concentration in the wash step can be
5 selected from a low stringency of about 2.0 x SSC at 50 °C to a high stringency of about 0.2 x SSC at 50 °C. In addition, the temperature in the wash step can be increased from low stringency conditions at room temperature, about 22 °C, to high stringency conditions at about 65 °C. Both temperature and salt may be varied, or temperature or salt concentration may be held constant while the other variable is
10 changed. In a preferred embodiment, a nucleic acid of the present invention will bind to one of SEQ ID Nos. 1-168, preferably SEQ ID Nos. 1-35, or a sequence complementary thereto, under moderately stringent conditions, for example at about 2.0 x SSC and about 40 °C. In a particularly preferred embodiment, a nucleic acid of the present invention will bind to one of SEQ ID Nos. 1-168, preferably SEQ ID Nos.
15 1-35, or a sequence complementary thereto, under high stringency conditions.

In one embodiment, the invention provides nucleic acids which hybridize under low stringency conditions of 6 x SSC at room temperature followed by a wash at 2 x SSC at room temperature.

In another embodiment, the invention provides nucleic acids which hybridize
20 under high stringency conditions of 2 x SSC at 65 °C followed by a wash at 0.2 x SSC at 65 °C.

Nucleic acids having a sequence that differs from the nucleotide sequences shown in one of SEQ ID Nos. 1-168, preferably SEQ ID Nos. 1-35, or a sequence complementary thereto, due to degeneracy in the genetic code, are also within the
25 scope of the invention. Such nucleic acids encode functionally equivalent peptides (i.e., a peptide having equivalent or similar biological activity) but differ in sequence from the sequence shown in the sequence listing due to degeneracy in the genetic code. For example, a number of amino acids are designated by more than one triplet. Codons that specify the same amino acid, or synonyms (for example, CAU and CAC
30 each encode histidine) may result in "silent" mutations which do not affect the amino acid sequence of a polypeptide. However, it is expected that DNA sequence polymorphisms that do lead to changes in the amino acid sequences of the subject polypeptides will exist among mammals. One skilled in the art will appreciate that

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these variations in one or more nucleotides (e.g., up to about 3-5% of the nucleotides) of the nucleic acids encoding polypeptides having an activity of a polypeptide may exist among individuals of a given species due to natural allelic variation.

Also within the scope of the invention are nucleic acids encoding splicing
5 variants of proteins encoded by a nucleic acid of SEQ ID Nos. 1-544, preferably SEQ ID Nos. 1-168, even more preferably SEQ ID Nos. 1-35, or a sequence complementary thereto, or natural homologs of such proteins. Such homologs can be cloned by hybridization or PCR, as further described herein.

The polynucleotide sequence may also encode for a leader sequence, e.g., the
10 natural leader sequence or a heterologous leader sequence, for a subject polypeptide. For example, the desired DNA sequence may be fused in the same reading frame to a DNA sequence which aids in expression and secretion of the polypeptide from the host cell, for example, a leader sequence which functions as a secretory sequence for controlling transport of the polypeptide from the cell. The protein having a leader
15 sequence is a preprotein and may have the leader sequence cleaved by the host cell to form the mature form of the protein.

The polynucleotide of the present invention may also be fused in frame to a marker sequence, also referred to herein as "Tag sequence" encoding a "Tag peptide", which allows for marking and/or purification of the polypeptide of the present
20 invention. In a preferred embodiment, the marker sequence is a hexahistidine tag, e.g., supplied by a PQE-9 vector. Numerous other Tag peptides are available commercially. Other frequently used Tags include myc-epitopes (e.g., see Ellison et al. (1991) *J Biol Chem* 266:21150-21157) which includes a 10-residue sequence from c-myc, the pFLAG system (International Biotechnologies, Inc.), the pEZZ-protein A
25 system (Pharmacia, NJ), and a 16 amino acid portion of the *Haemophilus influenza* hemagglutinin protein. Furthermore, any polypeptide can be used as a Tag so long as a reagent, e.g., an antibody interacting specifically with the Tag polypeptide is available or can be prepared or identified.

As indicated by the examples set out below, nucleic acids can be obtained
30 from mRNA present in any of a number of eukaryotic cells, e.g., and are preferably obtained from metazoan cells, more preferably from vertebrate cells, and even more preferably from mammalian cells. It should also be possible to obtain nucleic acids of the present invention from genomic DNA from both adults and embryos. For

example, a gene can be cloned from either a cDNA or a genomic library in accordance with protocols generally known to persons skilled in the art. cDNA can be obtained by isolating total mRNA from a cell, e.g., a vertebrate cell, a mammalian cell, or a human cell, including embryonic cells. Double stranded cDNAs can then be prepared from
5 the total mRNA, and subsequently inserted into a suitable plasmid or bacteriophage vector using any one of a number of known techniques. The gene can also be cloned using established polymerase chain reaction techniques in accordance with the nucleotide sequence information provided by the invention.

In certain embodiments, a nucleic acid, probe, vector, or other construct of the
10 present invention includes at least about five, at least about ten, or at least about twenty nucleic acids from a region designated as novel in Table 2. In certain other embodiments, a nucleic acid of the present invention includes at least about five, at least about ten, or at least about twenty nucleic acids which are not included in the clones whose accession numbers are listed in Table 2.

15 The invention includes within its scope a polynucleotide having the nucleotide sequence of nucleic acid obtained from this biological material, wherein the nucleic acid hybridizes under stringent conditions (at least about 4 x SSC at 65 °C, or at least about 4 x SSC at 42 °C; see, for example, U.S. Patent No. 5,707,829, incorporated herein by reference) with at least 15 contiguous nucleotides of at least one of SEQ ID
20 Nos. 1-544. By this is intended that when at least 15 contiguous nucleotides of one of SEQ ID Nos. 1-544 is used as a probe, the probe will preferentially hybridize with a gene or mRNA (of the biological material) comprising the complementary sequence, allowing the identification and retrieval of the nucleic acids of the biological material that uniquely hybridize to the selected probe. Probes from more than one of SEQ ID
25 Nos. 1-544 will hybridize with the same gene or mRNA if the cDNA from which they were derived corresponds to one mRNA. Probes of more than 15 nucleotides can be used, but 15 nucleotides represents enough sequence for unique identification.

Because the present nucleic acids represent partial mRNA transcripts, two or more nucleic acids of the invention may represent different regions of the same
30 mRNA transcript and the same gene. Thus, if two or more of SEQ ID Nos. 1-544 are identified as belonging to the same clone, then either sequence can be used to obtain the full-length mRNA or gene.

Nucleic acid-related polynucleotides can also be isolated from cDNA libraries. These libraries are preferably prepared from mRNA of human colon cells, more preferably, human colon cancer specific tissue, designated as the DE clones in the appended Tables. In another embodiment the nucleic acids are isolated from libraries
5 prepared from normal colon specific tissue, designated herein as PA clones in the appended Tables. In yet another embodiment, this invention discloses nucleic acid sequences that can be isolated from both libraries prepared from a human colon adenocarcinoma cell line, SW480, as well as from libraries prepared from either normal colon specific tissue or from colon cancer specific tissue. These sequences are
10 listed in Table 3. Alignment of SEQ ID Nos. 1-544, as described above, can indicate that a cell line or tissue source of a related protein or polynucleotide can also be used as a source of the nucleic acid-related cDNA.

Techniques for producing and probing nucleic acid sequence libraries are described, for example, in Sambrook *et al.*, "Molecular Cloning: A Laboratory
15 Manual" (New York, Cold Spring Harbor Laboratory, 1989). The cDNA can be prepared by using primers based on a sequence from SEQ ID Nos. 1-544. In one embodiment, the cDNA library can be made from only poly-adenylated mRNA. Thus, poly-T primers can be used to prepare cDNA from the mRNA. Alignment of SEQ ID Nos. 1-544 can result in identification of a related polypeptide or
20 polynucleotide. Some of the polynucleotides disclosed herein contains repetitive regions that were subject to masking during the search procedures. The information about the repetitive regions is discussed below.

Constructs of polynucleotides having sequences of SEQ ID Nos. 1-544 can be generated synthetically. Alternatively, single-step assembly of a gene and entire
25 plasmid from large numbers of oligodeoxyribonucleotides is described by Stemmer *et al.*, *Gene (Amsterdam)* (1995) 164(1):49-53. In this method, assembly PCR (the synthesis of long DNA sequences from large numbers of oligodeoxyribonucleotides (oligos)) is described. The method is derived from DNA shuffling (Stemmer, *Nature* (1994) 370:389-391), and does not rely on DNA ligase, but instead relies on DNA
30 polymerase to build increasingly longer DNA fragments during the assembly process. For example, a 1.1-kb fragment containing the TEM-1 beta-lactamase-encoding gene (bla) can be assembled in a single reaction from a total of 56 oligos, each 40 nucleotides (nt) in length. The synthetic gene can be PCR amplified and cloned in a

vector containing the tetracycline-resistance gene (Tc-R) as the sole selectable marker. Without relying on ampicillin (Ap) selection, 76% of the Tc-R colonies were Ap-R, making this approach a general method for the rapid and cost-effective synthesis of any gene.

5

IV. Identification of Functional and Structural Motifs of Novel-Genes Using Art-Recognized Methods

Translations of the nucleotide sequence of the nucleic acids, cDNAs, or full
10 genes can be aligned with individual known sequences. Similarity with individual sequences can be used to determine the activity of the polypeptides encoded by the polynucleotides of the invention. For example, sequences that show similarity with a chemokine sequence may exhibit chemokine activities. Also, sequences exhibiting similarity with more than one individual sequence may exhibit activities that are
15 characteristic of either or both individual sequences.

The full length sequences and fragments of the polynucleotide sequences of the nearest neighbors can be used as probes and primers to identify and isolate the full length sequence of the nucleic acid. The nearest neighbors can indicate a tissue or cell type to be used to construct a library for the full-length sequences of the nucleic acid.

20 Typically, the nucleic acids are translated in all six frames to determine the best alignment with the individual sequences. The sequences disclosed herein in the Sequence Listing are in a 5' to 3' orientation and translation in three frames can be sufficient (with a few specific exceptions as described in the Examples). These amino acid sequences are referred to, generally, as query sequences, which will be aligned
25 with the individual sequences.

Nucleic acid sequences can be compared with known genes by any of the methods disclosed above. Results of individual and query sequence alignments can be divided into three categories: high similarity, weak similarity, and no similarity. Individual alignment results ranging from high similarity to weak similarity provide a
30 basis for determining polypeptide activity and/or structure.

Parameters for categorizing individual results include: percentage of the alignment region length where the strongest alignment is found, percent sequence identity, and p value.

The percentage of the alignment region length is calculated by counting the number of residues of the individual sequence found in the region of strongest alignment. This number is divided by the total residue length of the query sequence to find a percentage. An example is shown below:

5

Query sequence:	ASNPERTMIPVTRVGLIRYM
Individual sequence:	YMMTEYLAIPV.RVGLPRYM
	1 5 10 15

10

The region of alignment begins at amino acid 9 and ends at amino acid 19. The total length of the query sequence is 20 amino acids. The percent of the alignment region length is $11/20$ or 55%.

Percent sequence identity is calculated by counting the number of amino acid matches between the query and individual sequence and dividing total number of matches by the number of residues of the individual sequence found in the region of strongest alignment. For the example above, the percent identity would be 10 matches divided by 11 amino acids, or approximately 90.9%.

P value is the probability that the alignment was produced by chance. For a single alignment, the p value can be calculated according to Karlin *et al.*, Proc. Natl. Acad. Sci. 87: 2264 (1990) and Karlin *et al.*, Proc. Natl. Acad. Sci. 90: (1993). The p value of multiple alignments using the same query sequence can be calculated using an heuristic approach described in Altschul *et al.*, Nat. Genet. 6: 119 (1994). Alignment programs such as BLAST program can calculate the p value.

The boundaries of the region where the sequences align can be determined according to Doolittle, *Methods in Enzymology*, *supra*; BLAST or FASTA programs; or by determining the area where the sequence identity is highest.

Another factor to consider for determining identity or similarity is the location of the similarity or identity. Strong local alignment can indicate similarity even if the length of alignment is short. Sequence identity scattered throughout the length of the query sequence also can indicate a similarity between the query and profile sequences.

High Similarity

For the alignment results to be considered high similarity, the percent of the alignment region length, typically, is at least about 55% of total length query sequence; more typically, at least about 58%; even more typically; at least about 60%
5 of the total residue length of the query sequence. Usually, percent length of the alignment region can be as much as about 62%; more usually, as much as about 64%; even more usually, as much as about 66%.

Further, for high similarity, the region of alignment, typically, exhibits at least about 75% of sequence identity; more typically, at least about 78%; even more
10 typically; at least about 80% sequence identity. Usually, percent sequence identity can be as much as about 82%; more usually, as much as about 84%; even more usually, as much as about 86%.

The p value is used in conjunction with these methods. If high similarity is found, the query sequence is considered to have high similarity with a profile
15 sequence when the p value is less than or equal to about 10^{-2} ; more usually; less than or equal to about 10^{-3} ; even more usually; less than or equal to about 10^{-4} . More typically, the p value is no more than about 10^{-5} ; more typically; no more than or equal to about 10^{-10} ; even more typically; no more than or equal to about 10^{-15} for the query sequence to be considered high similarity.

20

Weak Similarity

For the alignment results to be considered weak similarity, there is no minimum percent length of the alignment region nor minimum length of alignment. A better showing of weak similarity is considered when the region of alignment is,
25 typically, at least about 15 amino acid residues in length; more typically, at least about 20; even more typically; at least about 25 amino acid residues in length. Usually, length of the alignment region can be as much as about 30 amino acid residues; more usually, as much as about 40; even more usually, as much as about 60 amino acid residues.

30 Further, for weak similarity, the region of alignment, typically, exhibits at least about 35% of sequence identity; more typically, at least about 40%; even more typically; at least about 45% sequence identity. Usually, percent sequence identity

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can be as much as about 50%; more usually, as much as about 55%; even more usually, as much as about 60%.

If low similarity is found, the query sequence is considered to have weak similarity with a profile sequence when the p value is usually less than or equal to about 10^{-2} ; more usually; less than or equal to about 10^{-3} ; even more usually; less than or equal to about 10^{-4} . More typically, the p value is no more than about 10^{-5} ; more usually; no more than or equal to about 10^{-10} ; even more usually; no more than or equal to about 10^{-15} for the query sequence to be considered weak similarity.

10 Similarity Determined by Sequence Identity

Sequence identity alone can be used to determine similarity of a query sequence to an individual sequence and can indicate the activity of the sequence. Such an alignment, preferably, permits gaps to align sequences. Typically, the query sequence is related to the profile sequence if the sequence identity over the entire query sequence is at least about 15%; more typically, at least about 20%; even more typically, at least about 25%; even more typically, at least about 50%. Sequence identity alone as a measure of similarity is most useful when the query sequence is usually, at least 80 residues in length; more usually, 90 residues; even more usually, at least 95 amino acid residues in length. More typically, similarity can be concluded based on sequence identity alone when the query sequence is preferably 100 residues in length; more preferably, 120 residues in length; even more preferably, 150 amino acid residues in length.

Determining Activity from Alignments with Profile and Multiple Aligned Sequences

25 Translations of the nucleic acids can be aligned with amino acid profiles that define either protein families or common motifs. Also, translations of the nucleic acids can be aligned to multiple sequence alignments (MSA) comprising the polypeptide sequences of members of protein families or motifs. Similarity or identity with profile sequences or MSAs can be used to determine the activity of the polypeptides encoded by nucleic acids or corresponding cDNA or genes. For example, sequences that show an identity or similarity with a chemokine profile or MSA can exhibit chemokine activities.

Profiles can be designed manually by (1) creating a MSA, which is an alignment of the amino acid sequence of members that belong to the family and (2) constructing

a statistical representation of the alignment. Such methods are described, for example, in Birney *et al.*, Nucl. Acid Res. 24(14): 2730-2739 (1996).

MSAs of some protein families and motifs are publicly available. For example, these include MSAs of 547 different families and motifs. These MSAs are
5 described also in Sonnhammer *et al.*, Proteins 28: 405-420 (1997). Other sources are also available in the world wide web. A brief description of these MSAs is reported in Pascarella *et al.*, Prot. Eng. 9(3): 249-251 (1996).

Techniques for building profiles from MSAs are described in Sonnhammer *et al.*, *supra*; Birney *et al.*, *supra*; and Methods in Enzymology, vol. 266: "Computer
10 Methods for Macromolecular Sequence Analysis," 1996, ed. Doolittle, Academic Press, Inc., a division of Harcourt Brace & Co., San Diego, California, USA.

Similarity between a query sequence and a protein family or motif can be determined by (a) comparing the query sequence against the profile and/or (b) aligning the query sequence with the members of the family or motif.

15 Typically, a program such as Searchwise can be used to compare the query sequence to the statistical representation of the multiple alignment, also known as a profile. The program is described in Birney *et al.*, *supra*. Other techniques to compare the sequence and profile are described in Sonnhammer *et al.*, *supra* and Doolittle, *supra*.

20 Next, methods described by Feng *et al.*, J. Mol. Evol. 25: 351-360 (1987) and Higgins *et al.*, CABIOS 5: 151-153 (1989) can be used align the query sequence with the members of a family or motif, also known as a MSA. Computer programs, such as PILEUP, can be used. See Feng *et al.*, *infra*.

The following factors are used to determine if a similarity between a query
25 sequence and a profile or MSA exists: (1) number of conserved residues found in the query sequence, (2) percentage of conserved residues found in the query sequence, (3) number of frameshifts, and (4) spacing between conserved residues.

Some alignment programs that both translate and align sequences can make any number of frameshifts when translating the nucleotide sequence to produce the
30 best alignment. The fewer frameshifts needed to produce an alignment, the stronger the similarity or identity between the query and profile or MSAs. For example, a weak similarity resulting from no frameshifts can be a better indication of activity or structure of a query sequence, than a strong similarity resulting from two frameshifts.

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Preferably, three or fewer frameshifts are found in an alignment; more preferably two or fewer frameshifts; even more preferably, one or fewer frameshifts; even more preferably, no frameshifts are found in an alignment of query and profile or MSAs.

Conserved residues are those amino acids that are found at a particular
5 position in all or some of the family or motif members. For example, most known chemokines contain four conserved cysteines. Alternatively, a position is considered conserved if only a certain class of amino acids is found in a particular position in all or some of the family members. For example, the N-terminal position may contain a positively charged amino acid, such as lysine, arginine, or histidine.
10 Typically, a residue of a polypeptide is conserved when a class of amino acids or a single amino acid is found at a particular position in at least about 40% of all class members; more typically, at least about 50%; even more typically, at least about 60% of the members. Usually, a residue is conserved when a class or single amino acid is found in at least about 70% of the members of a family or motif; more usually,
15 at least about 80%; even more usually, at least about 90%; even more usually, at least about 95%.

A residue is considered conserved when three unrelated amino acids are found at a particular position in the some or all of the members; more usually, two unrelated amino acids. These residues are conserved when the unrelated amino acids are found
20 at particular positions in at least about 40% of all class member; more typically, at least about 50%; even more typically, at least about 60% of the members. Usually, a residue is conserved when a class or single amino acid is found in at least about 70% of the members of a family or motif; more usually, at least about 80%; even more usually, at least about 90%; even more usually, at least about 95%.

A query sequence has similarity to a profile or MSA when the query sequence comprises at least about 25% of the conserved residues of the profile or MSA; more usually, at least about 30%; even more usually; at least about 40%. Typically, the query sequence has a stronger similarity to a profile sequence or MSA when the query sequence comprises at least about 45% of the conserved residues of the profile or
30 MSA; more typically, at least about 50%; even more typically; at least about 55%.

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V. Probes and Primers

The nucleotide sequences determined from the cloning of genes from tumor cells, especially colon cancer cell lines and tissues will further allow for the generation of probes and primers designed for identifying and/or cloning homologs in other cell types, e.g., from other tissues, as well as homologs from other mammalian organisms. Nucleotide sequences useful as probes/primers may include all or a portion of the sequences listed in SEQ ID Nos. 1-544 or sequences complementary thereto or sequences which hybridize under stringent conditions to all or a portion of SEQ ID Nos. 1-544. For instance, the present invention also provides a probe/primer comprising a substantially purified oligonucleotide, which oligonucleotide comprising a nucleotide sequence that hybridizes under stringent conditions to at least approximately 12, preferably 25, more preferably 40, 50, or 75 consecutive nucleotides up to the full length of the sense or anti-sense sequence selected from the group consisting of SEQ ID Nos. 1-544, preferably SEQ ID Nos. 1-168, even more preferably SEQ ID Nos. 1-35, or a sequence complementary thereto, or naturally occurring mutants thereof. For instance, primers based on a nucleic acid represented in SEQ ID Nos. 1-544, preferably SEQ ID Nos. 1-168, even more preferably SEQ ID Nos. 1-35, or a sequence complementary thereto, can be used in PCR reactions to clone homologs of that sequence.

In yet another embodiment, the invention provides probes/primers comprising a nucleotide sequence that hybridizes under moderately stringent conditions to at least approximately 12, 16, 25, 40, 50 or 75 consecutive nucleotides up to the full length of the sense or antisense sequence selected from the group consisting of SEQ ID Nos. 1-544, preferably SEQ ID Nos. 1-168, even more preferably SEQ ID Nos. 1-35, or naturally occurring mutants thereof.

In particular, these probes are useful because they provide a method for detecting mutations in wild-type genes of the present invention. Nucleic acid probes which are complementary to a wild-type gene of the present invention and can form mismatches with mutant genes are provided, allowing for detection by enzymatic or chemical cleavage or by shifts in electrophoretic mobility.

Likewise, probes based on the subject sequences can be used to detect transcripts or genomic sequences encoding the same or homologous proteins, for use, for example, in prognostic or diagnostic assays. In preferred embodiments, the probe

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Full-length cDNA molecules comprising the disclosed nucleic acids are

Members of the library that are larger than the nucleic acid, and preferably that contain the whole sequence of the native message, may be obtained. To confirm that the entire cDNA has been obtained, RNA protection experiments may be performed as follows. Hybridization of a full-length cDNA to an mRNA may protect the RNA from RNase degradation. If the cDNA is not full length, then the portions of the mRNA that are not hybridized may be subject to RNase degradation. This may be assayed, as is known in the art, by changes in electrophoretic mobility on polyacrylamide gels, or by detection of released monoribonucleotides. Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, 2nd Ed. (Cold Spring Harbor Press, Cold Spring Harbor, NY 1989). In order to obtain additional sequences 5' to the end

of a partial cDNA, 5' RACE (PCR Protocols: A Guide to Methods and Applications (Academic Press, Inc. 1990)) may be performed.

Genomic DNA may be isolated using nucleic acids in a manner similar to the isolation of full-length cDNAs. Briefly, the nucleic acids, or portions thereof, may be used as probes to libraries of genomic DNA. Preferably, the library is obtained from the cell type that was used to generate the nucleic acids. Most preferably, the genomic DNA is obtained from the biological material described herein in the Example. Such libraries may be in vectors suitable for carrying large segments of a genome, such as P1 or YAC, as described in detail in Sambrook *et al.*, 9.4-9.30. In addition, genomic sequences can be isolated from human BAC libraries, which are commercially available from Research Genetics, Inc., Huntsville, Alabama, USA, for example. In order to obtain additional 5' or 3' sequences, chromosome walking may be performed, as described in Sambrook *et al.*, such that adjacent and overlapping fragments of genomic DNA are isolated. These may be mapped and pieced together, as is known in the art, using restriction digestion enzymes and DNA ligase.

Using the nucleic acids of the invention, corresponding full length genes can be isolated using both classical and PCR methods to construct and probe cDNA libraries. Using either method, Northern blots, preferably, may be performed on a number of cell types to determine which cell lines express the gene of interest at the highest rate.

Classical methods of constructing cDNA libraries are taught in Sambrook *et al.*, supra. With these methods, cDNA can be produced from mRNA and inserted into viral or expression vectors. Typically, libraries of mRNA comprising poly(A) tails can be produced with poly(T) primers. Similarly, cDNA libraries can be produced using the instant sequences as primers.

PCR methods may be used to amplify the members of a cDNA library that comprise the desired insert. In this case, the desired insert may contain sequence from the full length cDNA that corresponds to the instant nucleic acids. Such PCR methods include gene trapping and RACE methods.

Gene trapping may entail inserting a member of a cDNA library into a vector. The vector then may be denatured to produce single stranded molecules. Next, a substrate-bound probe, such a biotinylated oligo, may be used to trap cDNA inserts of interest. Biotinylated probes can be linked to an avidin-bound solid substrate. PCR

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methods can be used to amplify the trapped cDNA. To trap sequences corresponding to the full length genes, the labeled probe sequence may be based on the nucleic acids of the invention, e.g., SEQ ID Nos. 1-168, preferably SEQ ID Nos. 1-35, or a sequence complementary thereto. Random primers or primers specific to the library
5 vector can be used to amplify the trapped cDNA. Such gene trapping techniques are described in Gruber *et al.*, PCT WO 95/04745 and Gruber *et al.*, U.S. Pat. No. 5,500,356. Kits are commercially available to perform gene trapping experiments from, for example, Life Technologies, Gaithersburg, Maryland, USA.

“Rapid amplification of cDNA ends,” or RACE, is a PCR method of
10 amplifying cDNAs from a number of different RNAs. The cDNAs may be ligated to an oligonucleotide linker and amplified by PCR using two primers. One primer may be based on sequence from the instant nucleic acids, for which full length sequence is desired, and a second primer may comprise a sequence that hybridizes to the oligonucleotide linker to amplify the cDNA. A description of this method is reported
15 in PCT Pub. No. WO 97/19110.

In preferred embodiments of RACE, a common primer may be designed to anneal to an arbitrary adaptor sequence ligated to cDNA ends (Apte and Siebert, Biotechniques 15:890-893, 1993; Edwards *et al.*, Nuc. Acids Res. 19:5227-5232, 1991). When a single gene-specific RACE primer is paired with the common primer,
20 preferential amplification of sequences between the single gene specific primer and the common primer occurs. Commercial cDNA pools modified for use in RACE are available.

Another PCR-based method generates full-length cDNA library with anchored ends without specific knowledge of the cDNA sequence. The method uses lock-
25 docking primers (I-VI), where one primer, poly TV (I-III) locks over the polyA tail of eukaryotic mRNA producing first strand synthesis and a second primer, polyGH (IV-VI) locks onto the polyC tail added by terminal deoxynucleotidyl transferase (TdT). This method is described in PCT Pub. No. WO 96/40998.

The promoter region of a gene generally is located 5' to the initiation site for
30 RNA polymerase II. Hundreds of promoter regions contain the “TATA” box, a sequence such as TATTA or TATAA, which is sensitive to mutations. The promoter region can be obtained by performing 5' RACE using a primer from the coding region

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of the gene. Alternatively, the cDNA can be used as a probe for the genomic sequence, and the region 5' to the coding region is identified by "walking up."

If the gene is highly expressed or differentially expressed, the promoter from the gene may be of use in a regulatory construct for a heterologous gene.

5 Once the full-length cDNA or gene is obtained, DNA encoding variants can be prepared by site-directed mutagenesis, described in detail in Sambrook *et al.*, 15.3-15.63. The choice of codon or nucleotide to be replaced can be based on the disclosure herein on optional changes in amino acids to achieve altered protein structure and/or function.

10 As an alternative method to obtaining DNA or RNA from a biological material, nucleic acid comprising nucleotides having the sequence of one or more nucleic acids of the invention can be synthesized. Thus, the invention encompasses nucleic acid molecules ranging in length from 12 nucleotides (corresponding to at least 12 contiguous nucleotides which hybridize under stringent conditions to or are at
15 least 80% identical to a nucleic acid represented by one of SEQ ID Nos. 1-544, preferably SEQ ID Nos. 1-168, even more preferably SEQ ID Nos. 1-35, or a sequence complementary thereto) up to a maximum length suitable for one or more biological manipulations, including replication and expression, of the nucleic acid molecule. The invention includes but is not limited to (a) nucleic acid having the size
20 of a full gene, and comprising at least one of SEQ ID Nos. 1-544, preferably SEQ ID Nos. 1-168, even more preferably SEQ ID Nos. 1-35, or a sequence complementary thereto; (b) the nucleic acid of (a) also comprising at least one additional gene, operably linked to permit expression of a fusion protein; (c) an expression vector comprising (a) or (b); (d) a plasmid comprising (a) or (b); and (e) a recombinant viral
25 particle comprising (a) or (b). Construction of (a) can be accomplished as described below in part IV.

 The sequence of a nucleic acid of the present invention is not limited and can be any sequence of A, T, G, and/or C (for DNA) and A, U, G, and/or C (for RNA) or modified bases thereof, including inosine and pseudouridine. The choice of sequence
30 will depend on the desired function and can be dictated by coding regions desired, the intron-like regions desired, and the regulatory regions desired.

VI. Vectors Carrying Nucleic Acids of the Present Invention

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The invention further provides plasmids and vectors, which can be used to express a gene in a host cell. The host cell may be any prokaryotic or eukaryotic cell. Thus, a nucleotide sequence derived from any one of SEQ ID Nos. 1-544, preferably SEQ ID Nos. 1-168, even more preferably SEQ ID Nos. 1-35, or a sequence
5 complementary thereto, encoding all or a selected portion of a protein, can be used to produce a recombinant form of an polypeptide via microbial or eukaryotic cellular processes. Ligating the polynucleotide sequence into a gene construct, such as an expression vector, and transforming or transfecting into hosts, either eukaryotic (yeast, avian, insect or mammalian) or prokaryotic (bacterial cells), are standard
10 procedures well known in the art.

Vectors that allow expression of a nucleic acid in a cell are referred to as expression vectors. Typically, expression vectors contain a nucleic acid operably linked to at least one transcriptional regulatory sequence. Regulatory sequences are art-recognized and are selected to direct expression of the subject nucleic acids.
15 Transcriptional regulatory sequences are described in Goeddel; Gene Expression Technology: Methods in Enzymology 185, Academic Press, San Diego, CA (1990). In one embodiment, the expression vector includes a recombinant gene encoding a peptide having an agonistic activity of a subject polypeptide, or alternatively, encoding a peptide which is an antagonistic form of a subject polypeptide.

20 The choice of plasmid will depend on the type of cell in which propagation is desired and the purpose of propagation. Certain vectors are useful for amplifying and making large amounts of the desired DNA sequence. Other vectors are suitable for expression in cells in culture. Still other vectors are suitable for transfer and expression in cells in a whole animal or person. The choice of appropriate vector is
25 well within the skill of the art. Many such vectors are available commercially. The nucleic acid or full-length gene is inserted into a vector typically by means of DNA ligase attachment to a cleaved restriction enzyme site in the vector. Alternatively, the desired nucleotide sequence may be inserted by homologous recombination in vivo. Typically this is accomplished by attaching regions of homology to the vector on the
30 flanks of the desired nucleotide sequence. Regions of homology are added by ligation of oligonucleotides, or by polymerase chain reaction using primers comprising both the region of homology and a portion of the desired nucleotide sequence.

Nucleic acids or full-length genes are linked to regulatory sequences as appropriate to obtain the desired expression properties. These may include promoters (attached either at the 5' end of the sense strand or at the 3' end of the antisense strand), enhancers, terminators, operators, repressors, and inducers. The promoters
5 may be regulated or constitutive. In some situations it may be desirable to use conditionally active promoters, such as tissue-specific or developmental stage-specific promoters. These are linked to the desired nucleotide sequence using the techniques described above for linkage to vectors. Any techniques known in the art may be used.

When any of the above host cells, or other appropriate host cells or organisms,
10 are used to replicate and/or express the polynucleotides or nucleic acids of the invention, the resulting replicated nucleic acid, RNA, expressed protein or polypeptide, is within the scope of the invention as a product of the host cell or organism. The product is recovered by any appropriate means known in the art.

Once the gene corresponding to the nucleic acid is identified, its expression
15 can be regulated in the cell to which the gene is native. For example, an endogenous gene of a cell can be regulated by an exogenous regulatory sequence as disclosed in U.S. Patent No. 5,641,670, "Protein Production and Protein Delivery."

A number of vectors exist for the expression of recombinant proteins in yeast (see, for example, Broach *et al.* (1983) in *Experimental Manipulation of Gene
20 Expression*, ed. M. Inouye, Academic Press, p. 83, incorporated by reference herein). In addition, drug resistance markers such as ampicillin can be used. In an illustrative embodiment, a polypeptide is produced recombinantly utilizing an expression vector generated by sub-cloning one of the nucleic acids represented in one of SEQ ID Nos. 1-544, preferably SEQ ID Nos. 1-168, even more preferably SEQ ID Nos. 1-35, or a
25 sequence complementary thereto.

The preferred mammalian expression vectors contain both prokaryotic sequences, to facilitate the propagation of the vector in bacteria, and one or more eukaryotic transcription units that are expressed in eukaryotic cells. The various methods employed in the preparation of plasmids and transformation of host
30 organisms are well known in the art. For other suitable expression systems for both prokaryotic and eukaryotic cells, as well as general recombinant procedures, see *Molecular Cloning: A Laboratory Manual*, 2nd Ed., ed. by Sambrook, Fritsch and Maniatis (Cold Spring Harbor Laboratory Press: 1989) Chapters 16 and 17.

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When it is desirable to express only a portion of a gene, e.g., a truncation mutant, it may be necessary to add a start codon (ATG) to the oligonucleotide fragment containing the desired sequence to be expressed. It is well known in the art that a methionine at the N-terminal position can be enzymatically cleaved by the use of the enzyme methionine aminopeptidase (MAP). MAP has been cloned from *E. coli* (Ben-Bassat *et al.* (1987) *J. Bacteriol.* 169:751-757) and *Salmonella typhimurium* and its *in vitro* activity has been demonstrated on recombinant proteins (Miller *et al.* (1987) *PNAS* 84:2718-1722). Therefore, removal of an N-terminal methionine, if desired, can be achieved either *in vivo* by expressing polypeptides in a host which produces MAP (e.g., *E. coli* or CM89 or *S. cerevisiae*), or *in vitro* by use of purified MAP (e.g., procedure of Miller *et al.*, *supra*).

Moreover, the nucleic acid constructs of the present invention can also be used as part of a gene therapy protocol to deliver nucleic acids such as antisense nucleic acids. Thus, another aspect of the invention features expression vectors for *in vivo* or *in vitro* transfection with an antisense oligonucleotide.

In addition to viral transfer methods, non-viral methods can also be employed to introduce a subject nucleic acid, e.g., a sequence represented by one of SEQ ID Nos. 1-544, preferably SEQ ID Nos. 1-168, even more preferably SEQ ID Nos. 1-35, or a sequence complementary thereto, into the tissue of an animal. Most nonviral methods of gene transfer rely on normal mechanisms used by mammalian cells for the uptake and intracellular transport of macromolecules. In preferred embodiments, non-viral targeting means of the present invention rely on endocytic pathways for the uptake of the subject nucleic acid by the targeted cell. Exemplary targeting means of this type include liposomal derived systems, polylysine conjugates, and artificial viral envelopes.

A nucleic acid of any of SEQ ID Nos. 1-544, preferably SEQ ID Nos. 1-168, even more preferably SEQ ID Nos. 1-35, or a sequence complementary thereto, the corresponding cDNA, or the full-length gene may be used to express the partial or complete gene product. Appropriate nucleic acid constructs are purified using standard recombinant DNA techniques as described in, for example, Sambrook *et al.*, (1989) *Molecular Cloning: A Laboratory Manual*, 2nd ed. (Cold Spring Harbor Press, Cold Spring Harbor, New York), and under current regulations described in United States Dept. of HHS, National Institute of Health (NIH) Guidelines for Recombinant

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DNA Research. The polypeptides encoded by the nucleic acid may be expressed in any expression system, including, for example, bacterial, yeast, insect, amphibian and mammalian systems. Suitable vectors and host cells are described in U.S. Patent No. 5,654,173.

5 Bacteria. Expression systems in bacteria include those described in Chang *et al.*, *Nature* (1978) 275:615, Goeddel *et al.*, *Nature* (1979) 281:544; Goeddel *et al.*, *Nucleic Acids Res.* (1980) 8:4057; EP 0 036,776, U.S. Patent No. 4,551,433, DeBoer *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1983) 80:2125, and Siebenlist *et al.*, *Cell* (1980) 20:269.

10 Yeast. Expression systems in yeast include those described in Hinnen *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1978) 75:1929; Ito *et al.*, *J. Bacteriol.* (1983) 153:163; Kurtz *et al.*, *Mol. Cell. Biol.* (1986) 6:144; Kunze *et al.*, *J. Basic Microbiol.* (1985) 25:141; Gleeson *et al.*, *J. Gen. Microbiol.* (1986) 132:3459, Roggenkamp *et al.*, *Mol. Gen. Genet.* (1986) 202:302; Das *et al.*, *J. Bacteriol.* (1984) 158:1165; De
15 Louvencourt *et al.*, *J. Bacteriol.* (1983) 154:737, Van den Berg *et al.*, *Bio/Technology* (1990) 8:135; Kunze *et al.*, *J. Basic Microbiol.* (1985) 25:141; Cregg *et al.*, *Mol. Cell. Biol.* (1985) 5:3376, U.S. Patent Nos. 4,837,148 and 4,929,555; Beach and Nurse, *Nature* (1981) 300:706; Davidow *et al.*, *Curr. Genet.* (1985) 10:380, Gaillardin *et al.*, *Curr. Genet.* (1985) 10:49, Ballance *et al.*, *Biochem. Biophys. Res. Commun.* (1983)
20 112:284289; Tilburn *et al.*, *Gene* (1983) 26:205221, Yelton *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1984) 81:14701474, Kelly and Hynes, *EMBO J.* (1985) 4:475479; EP 0 244,234, and WO 91/00357.

Insect Cells. Expression of heterologous genes in insects is accomplished as described in U.S. Patent No. 4,745,051, Friesen *et al.* (1986) "The Regulation of
25 Baculovirus Gene Expression" in: *The Molecular Biology Of Baculoviruses* (W. Doerfler, ed.), EP 0 127,839, EP 0 155,476, and Vlak *et al.*, *J. Gen. Virol.* (1988) 69:765776, Miller *et al.*, *Ann. Rev. Microbiol.* (1988) 42:177, Carbonell *et al.*, *Gene* (1988) 73:409, Maeda *et al.*, *Nature* (1985) 315:592594, Lebacqz-Verheyden *et al.*, *Mol. Cell. Biol.* (1988) 8:3129; Smith *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1985)
30 82:8404, Miyajima *et al.*, *Gene* (1987) 58:273; and Martin *et al.*, *DNA* (1988) 7:99. Numerous baculoviral strains and variants and corresponding permissive insect host cells from hosts are described in Luckow *et al.*, *Bio/Technology* (1988) 6:4755, Miller

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et al., Generic Engineering (Setlow, J.K. *et al.* eds.), Vol. 8 (Plenum Publishing, 1986), pp. 277279, and Maeda *et al.*, *Nature*, (1985) 315:592-594.

Mammalian Cells. Mammalian expression is accomplished as described in Dijkema *et al.*, *EMBO J.* (1985) 4:761, Gorman *et al.*, *Proc. Natl. Acad. Sci. (USA)*

5 (1982) 79:6777, Boshart *et al.*, *Cell* (1985) 41:521 and U.S. Patent No. 4,399,216.

Other features of mammalian expression are facilitated as described in Ham and Wallace, *Meth. Enz.* (1979) 58:44, Barnes and Sato, *Anal. Biochem.* (1980) 102:255, U.S. Patent Nos. 4,767,704, 4,657,866, 4,927,762, 4,560,655, WO 90/103430, WO 87/00195, and U.S. RE 30,985.

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VII. Therapeutic Nucleic Acid Constructs

One aspect of the invention relates to the use of the isolated nucleic acid, e.g., SEQ ID Nos. 1-544, preferably SEQ ID Nos. 1-168, even more preferably SEQ ID Nos. 1-35, or a sequence complementary thereto, in antisense therapy. As used

15 herein, antisense therapy refers to administration or *in situ* generation of oligonucleotide molecules or their derivatives which specifically hybridize (e.g., bind) under cellular conditions with the cellular mRNA and/or genomic DNA, thereby inhibiting transcription and/or translation of that gene. The binding may be by conventional base pair complementarity, or, for example, in the case of binding to

20 DNA duplexes, through specific interactions in the major groove of the double helix. In general, antisense therapy refers to the range of techniques generally employed in the art, and includes any therapy which relies on specific binding to oligonucleotide sequences.

An antisense construct of the present invention can be delivered, for example,

25 as an expression plasmid which, when transcribed in the cell, produces RNA which is complementary to at least a unique portion of the cellular mRNA. Alternatively, the antisense construct is an oligonucleotide probe which is generated *ex vivo* and which, when introduced into the cell, causes inhibition of expression by hybridizing with the mRNA and/or genomic sequences of a subject nucleic acid. Such oligonucleotide

30 probes are preferably modified oligonucleotides which are resistant to endogenous nucleases, e.g., exonucleases and/or endonucleases, and are therefore stable *in vivo*. Exemplary nucleic acid molecules for use as antisense oligonucleotides are phosphoramidate, phosphorothioate and methylphosphonate analogs of DNA (see also

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U.S. Patents 5,176,996; 5,264,564; and 5,256,775). Additionally, general approaches to constructing oligomers useful in antisense therapy have been reviewed, for example, by Van der Krol et al. (1988) *BioTechniques* 6:958-976; and Stein et al. (1988) *Cancer Res* 48:2659-2668. With respect to antisense DNA,

- 5 oligodeoxyribonucleotides derived from the translation initiation site, e.g., between the -10 and +10 regions of the nucleotide sequence of interest, are preferred.

Antisense approaches involve the design of oligonucleotides (either DNA or RNA) that are complementary to mRNA. The antisense oligonucleotides will bind to the mRNA transcripts and prevent translation. Absolute complementarity, although
10 preferred, is not required. In the case of double-stranded antisense nucleic acids, a single strand of the duplex DNA may thus be tested, or triplex formation may be assayed. The ability to hybridize will depend on both the degree of complementarity and the length of the antisense nucleic acid. Generally, the longer the hybridizing nucleic acid, the more base mismatches with an RNA it may contain and still form a
15 stable duplex (or triplex, as the case may be). One skilled in the art can ascertain a tolerable degree of mismatch by use of standard procedures to determine the melting point of the hybridized complex.

Oligonucleotides that are complementary to the 5' "end of the mRNA, e.g., the 5' untranslated sequence up to and including the AUG initiation codon, should work
20 most efficiently at inhibiting translation. However, sequences complementary to the 3' untranslated sequences of mRNAs have recently been shown to be effective at inhibiting translation of mRNAs as well. (Wagner, R. 1994. *Nature* 372:333). Therefore, oligonucleotides complementary to either the 5' or 3' untranslated, non-coding regions of a gene could be used in an antisense approach to inhibit translation
25 of endogenous mRNA. Oligonucleotides complementary to the 5' untranslated region of the mRNA should include the complement of the AUG start codon. Antisense oligonucleotides complementary to mRNA coding regions are typically less efficient inhibitors of translation but could also be used in accordance with the invention. Whether designed to hybridize to the 5', 3', or coding region of subject mRNA,
30 antisense nucleic acids should be at least six nucleotides in length, and are preferably less than about 100 and more preferably less than about 50, 25, 17 or 10 nucleotides in length.

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Regardless of the choice of target sequence, it is preferred that *in vitro* studies are first performed to quantitate the ability of the antisense oligonucleotide to quantitate the ability of the antisense oligonucleotide to inhibit gene expression. It is preferred that these studies utilize controls that distinguish between antisense gene inhibition and nonspecific biological effects of oligonucleotides. It is also preferred that these studies compare levels of the target RNA or protein with that of an internal control RNA or protein. Additionally, it is envisioned that results obtained using the antisense oligonucleotide are compared with those obtained using a control oligonucleotide. It is preferred that the control oligonucleotide is of approximately the same length as the test oligonucleotide and that the nucleotide sequence of the oligonucleotide differs from the antisense sequence no more than is necessary to prevent specific hybridization to the target sequence.

The oligonucleotides can be DNA or RNA or chimeric mixtures or derivatives or modified versions thereof, single-stranded or double-stranded. The oligonucleotide can be modified at the base moiety, sugar moiety, or phosphate backbone, for example, to improve stability of the molecule, hybridization, etc. The oligonucleotide may include other appended groups such as peptides (e.g., for targeting host cell receptors), or agents facilitating transport across the cell membrane (see, e.g., Letsinger et al., 1989, Proc. Natl. Acad. Sci. U.S.A. 86:6553-6556; Lemaitre et al., 1987, Proc. Natl. Acad. Sci. 84:648-652; PCT Publication No. WO 88/09810, published December 15, 1988) or the blood-brain barrier (see, e.g., PCT Publication No. WO 89/10134, published April 25, 1988), hybridization-triggered cleavage agents (See, e.g., Krol et al., 1988, BioTechniques 6:958-976), or intercalating agents (See, e.g., Zon, 1988, Pharm. Res. 5:539-549). To this end, the oligonucleotide may be conjugated to another molecule, e.g., a peptide, hybridization triggered cross-linking agent, transport agent, hybridization-triggered cleavage agent, etc.

The antisense oligonucleotide may comprise at least one modified base moiety which is selected from the group including but not limited to 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xantine, 4-acetylcytosine, 5-(carboxyhydroxytriethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine,

7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine.

The antisense oligonucleotide may also comprise at least one modified sugar moiety selected from the group including but not limited to arabinose, 2-fluoroarabinose, xylulose, and hexose.

The antisense oligonucleotide can also contain a neutral peptide-like backbone. Such molecules are termed peptide nucleic acid (PNA)-oligomers and are described, e.g., in Perry- O'Keefe et al. (1996) Proc. Natl. Acad. Sci. U.S.A. 93:14670 and in Eglom *et al.* (1993) Nature 365:566. One advantage of PNA oligomers is their capability to bind to complementary DNA essentially independently from the ionic strength of the medium due to the neutral backbone of the DNA. In yet another embodiment, the antisense oligonucleotide comprises at least one modified phosphate backbone selected from the group consisting of a phosphorothioate, a phosphorodithioate, a phosphoramidothioate, a phosphoramidate, a phosphordiamidate, a methylphosphonate, an alkyl phosphotriester, and a formacetal or analog thereof.

In yet a further embodiment, the antisense oligonucleotide is an α -anomeric oligonucleotide. An α -anomeric oligonucleotide forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gautier et al., 1987, Nucl. Acids Res. 15:6625-6641). The oligonucleotide is a 2'-O-methylribonucleotide (Inoue et al., 1987, Nucl. Acids Res. 15:6131-6148), or a chimeric RNA-DNA analogue (Inoue et al., 1987, FEBS Lett. 215:327-330).

Oligonucleotides of the invention may be synthesized by standard methods known in the art, e.g., by use of an automated DNA synthesizer (such as are commercially available from Biosearch, Applied Biosystems, etc.). As examples, phosphorothioate oligonucleotides may be synthesized by the method of Stein et al. (1988, Nucl. Acids Res. 16:3209), methylphosphonate oligonucleotides can be

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prepared by use of controlled pore glass polymer supports (Sarin et al., 1988, Proc. Natl. Acad. Sci. U.S.A. 85:7448-7451), etc.

While antisense nucleotides complementary to a coding region sequence can be used, those complementary to the transcribed untranslated region and to the region
5 comprising the initiating methionine are most preferred.

The antisense molecules can be delivered to cells which express the target nucleic acid *in vivo*. A number of methods have been developed for delivering antisense DNA or RNA to cells; e.g., antisense molecules can be injected directly into the tissue site, or modified antisense molecules, designed to target the desired cells
10 (e.g., antisense linked to peptides or antibodies that specifically bind receptors or antigens expressed on the target cell surface) can be administered systemically.

However, it is often difficult to achieve intracellular concentrations of the antisense sufficient to suppress translation on endogenous mRNAs. Therefore, a preferred approach utilizes a recombinant DNA construct in which the antisense
15 oligonucleotide is placed under the control of a strong pol III or pol II promoter. The use of such a construct to transfect target cells in the patient will result in the transcription of sufficient amounts of single stranded RNAs that will form complementary base pairs with the endogenous transcripts and thereby prevent translation of the target mRNA. For example, a vector can be introduced *in vivo* such
20 that it is taken up by a cell and directs the transcription of an antisense RNA. Such a vector can remain episomal or become chromosomally integrated, as long as it can be transcribed to produce the desired antisense RNA. Such vectors can be constructed by recombinant DNA technology methods standard in the art. Vectors can be plasmid, viral, or others known in the art for replication and expression in mammalian cells.
25 Expression of the sequence encoding the antisense RNA can be by any promoter known in the art to act in mammalian, preferably human cells. Such promoters can be inducible or constitutive. Such promoters include but are not limited to: the SV40 early promoter region (Bernoist and Chambon, 1981, Nature 290:304-310), the promoter contained in the 3' long terminal repeat of Rous sarcoma virus (Yamamoto
30 *et al.*, 1980, Cell 22:787-797), the herpes thymidine kinase promoter (Wagner et al., 1981, Proc. Natl. Acad. Sci. U.S.A. 78:1441-1445), the regulatory sequences of the metallothionein gene (Brinster et al, 1982, Nature 296:39-42), etc. Any type of plasmid, cosmid, YAC or viral vector can be used to prepare the recombinant DNA

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construct which can be introduced directly into the tissue site; e.g., the choroid plexus or hypothalamus. Alternatively, viral vectors can be used which selectively infect the desired tissue (e.g., for brain, herpesvirus vectors may be used), in which case administration may be accomplished by another route (e.g., systemically).

5 In another aspect of the invention, ribozyme molecules designed to catalytically cleave target mRNA transcripts can be used to prevent translation of target mRNA and expression of a target protein (See, e.g., PCT International Publication WO90/11364, published October 4, 1990; Sarver *et al.*, 1990, Science 247:1222-1225 and U.S. Patent No. 5,093,246). While ribozymes that cleave mRNA
10 at site specific recognition sequences can be used to destroy target mRNAs, the use of hammerhead ribozymes is preferred. Hammerhead ribozymes cleave mRNAs at locations dictated by flanking regions that form complementary base pairs with the target mRNA. The sole requirement is that the target mRNA have the following sequence of two bases: 5'-UG-3'. The construction and production of hammerhead
15 ribozymes is well known in the art and is described more fully in Haseloff and Gerlach, 1988, Nature, 334:585-591. Preferably the ribozyme is engineered so that the cleavage recognition site is located near the 5' end of the target mRNA; i.e., to increase efficiency and minimize the intracellular accumulation of non-functional mRNA transcripts.

20 The ribozymes of the present invention also include RNA endoribonucleases (hereinafter "Cech-type ribozymes") such as the one which occurs naturally in *Tetrahymena thermophila* (known as the IVS, or L-19 IVS RNA) and which has been extensively described by Thomas Cech and collaborators (Zaug, et al., 1984, Science, 224:574-578; Zaug and Cech, 1986, Science, 231:470-475; Zaug, et al., 1986, Nature,
25 324:429-433; published International patent application No. WO88/04300 by University Patents Inc.; Been and Cech, 1986, Cell, 47:207-216). The Cech-type ribozymes have an eight base pair active site which hybridizes to a target RNA sequence whereafter cleavage of the target RNA takes place. The invention encompasses those Cech-type ribozymes which target eight base-pair active site
30 sequences that are present in a target gene.

As in the antisense approach, the ribozymes can be composed of modified oligonucleotides (e.g., for improved stability, targeting, etc.) and should be delivered to cells which express the target gene *in vivo*. A preferred method of delivery

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involves using a DNA construct "encoding" the ribozyme under the control of a strong constitutive pol III or pol II promoter, so that transfected cells will produce sufficient quantities of the ribozyme to destroy endogenous messages and inhibit translation. Because ribozymes, unlike antisense molecules, are catalytic, a lower
5 intracellular concentration is required for efficiency.

Antisense RNA, DNA, and ribozyme molecules of the invention may be prepared by any method known in the art for the synthesis of DNA and RNA molecules. These include techniques for chemically synthesizing oligodeoxyribonucleotides and oligoribonucleotides well known in the art such as for
10 example solid phase phosphoramidite chemical synthesis. Alternatively, RNA molecules may be generated by *in vitro* and *in vivo* transcription of DNA sequences encoding the antisense RNA molecule. Such DNA sequences may be incorporated into a wide variety of vectors which incorporate suitable RNA polymerase promoters such as the T7 or SP6 polymerase promoters. Alternatively, antisense cDNA
15 constructs that synthesize antisense RNA constitutively or inducibly, depending on the promoter used, can be introduced stably into cell lines.

Moreover, various well-known modifications to nucleic acid molecules may be introduced as a means of increasing intracellular stability and half-life. Possible modifications include but are not limited to the addition of flanking sequences of
20 ribonucleotides or deoxyribonucleotides to the 5' and/or 3' ends of the molecule or the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages within the oligodeoxyribonucleotide backbone.

VIII. Polypeptides of the Present Invention

25 The present invention makes available isolated polypeptides which are isolated from, or otherwise substantially free of other cellular proteins, especially other signal transduction factors and/or transcription factors which may normally be associated with the polypeptide. Subject polypeptides of the present invention include polypeptides encoded by the nucleic acids of SEQ ID Nos. 1-544, preferably SEQ ID
30 Nos. 1-168, even more preferably SEQ ID Nos. 1-35, or a sequence complementary thereto, or polypeptides encoded by genes of which a sequence in SEQ ID Nos. 1-544, preferably SEQ ID Nos. 1-168, even more preferably SEQ ID Nos. 1-35, or a sequence complementary thereto, is a fragment. Polypeptides of the present invention

include those proteins which are differentially regulated in tumor cells, especially colon cancer-derived cell lines (relative to normal cells, e.g., normal colon tissue and non-colon tissue). In preferred embodiments, the polypeptides are upregulated in tumor cells, especially colon cancer cancer-derived cell lines. In other embodiments, the polypeptides are downregulated in tumor cells, especially colon cancer-derived cell lines. Proteins which are upregulated, such as oncogenes, or downregulated, such as tumor suppressors, in aberrantly proliferating cells may be targets for diagnostic or therapeutic techniques. For example, upregulation of the *cdc2* gene induces mitosis. Overexpression of the *myt1* gene, a mitotic deactivator, negatively regulates the activity of *cdc2*. Aberrant proliferation may thus be induced either by upregulating *cdc2* or by downregulating *myt1*.

The term "substantially free of other cellular proteins" (also referred to herein as "contaminating proteins") or "substantially pure or purified preparations" are defined as encompassing preparations of polypeptides having less than about 20% (by dry weight) contaminating protein, and preferably having less than about 5% contaminating protein. Functional forms of the subject polypeptides can be prepared, for the first time, as purified preparations by using a cloned nucleic acid as described herein. Full length proteins or fragments corresponding to one or more particular motifs and/or domains or to arbitrary sizes, for example, at least about 5, 10, 25, 50, 75, or 100 amino acids in length are within the scope of the present invention.

For example, isolated polypeptides can be encoded by all or a portion of a nucleic acid sequence shown in any of SEQ ID Nos. 1-544, preferably SEQ ID Nos. 1-168, even more preferably SEQ ID Nos. 1-35, or a sequence complementary thereto. Isolated peptidyl portions of proteins can be obtained by screening peptides recombinantly produced from the corresponding fragment of the nucleic acid encoding such peptides. In addition, fragments can be chemically synthesized using techniques known in the art such as conventional Merrifield solid phase f-Moc or t-Boc chemistry. For example, a polypeptide of the present invention may be arbitrarily divided into fragments of desired length with no overlap of the fragments, or preferably divided into overlapping fragments of a desired length. The fragments can be produced (recombinantly or by chemical synthesis) and tested to identify those peptidyl fragments which can function as either agonists or antagonists of a wild-type (e.g., "authentic") protein.

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Another aspect of the present invention concerns recombinant forms of the subject proteins. Recombinant polypeptides preferred by the present invention, in addition to native proteins, as described above are encoded by a nucleic acid, which is at least 60%, more preferably at least 80%, and more preferably 85%, and more preferably 90%, and more preferably 95% identical to an amino acid sequence encoded by SEQ ID Nos. 1-544. Polypeptides which are encoded by a nucleic acid that is at least about 98-99% identical with the sequence of SEQ ID Nos. 1-544 are also within the scope of the invention. Also included in the present invention are peptide fragments comprising at least a portion of such a protein.

10 In a preferred embodiment, a polypeptide of the present invention is a mammalian polypeptide and even more preferably a human polypeptide. In particularly preferred embodiment, the polypeptide retains wild-type bioactivity. It will be understood that certain post-translational modifications, e.g., phosphorylation and the like, can increase the apparent molecular weight of the polypeptide relative to the unmodified polypeptide chain.

15 The present invention further pertains to recombinant forms of one of the subject polypeptides. Such recombinant polypeptides preferably are capable of functioning in one of either role of an agonist or antagonist of at least one biological activity of a wild-type ("authentic") polypeptide of the appended sequence listing. The term "evolutionarily related to", with respect to amino acid sequences of proteins, refers to both polypeptides having amino acid sequences which have arisen naturally, and also to mutational variants of human polypeptides which are derived, for example, by combinatorial mutagenesis.

25 In general, polypeptides referred to herein as having an activity (e.g., are "bioactive") of a protein are defined as polypeptides which include an amino acid sequence encoded by all or a portion of the nucleic acid sequences shown in one of SEQ ID Nos. 1-544, preferably SEQ ID Nos. 1-168, even more preferably SEQ ID Nos. 1-35, or a sequence complementary thereto, and which mimic or antagonize all or a portion of the biological/biochemical activities of a naturally occurring protein.

30 According to the present invention, a polypeptide has biological activity if it is a specific agonist or antagonist of a naturally occurring form of a protein.

Assays for determining whether a compound, e.g. a protein or variant thereof, has one or more of the above biological activities are well known in the art. In certain

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embodiments, the polypeptides of the present invention have activities such as those outlined above.

In another embodiment, the coding sequences for the polypeptide can be incorporated as a part of a fusion gene including a nucleotide sequence encoding a different polypeptide. This type of expression system can be useful under conditions where it is desirable to produce an immunogenic fragment of a polypeptide (see, for example, EP Publication No. 0259149; and Evans *et al.* (1989) *Nature* 339:385; Huang *et al.* (1988) *J. Virol.* 62:3855; and Schlienger *et al.* (1992) *J. Virol.* 66:2). In addition to utilizing fusion proteins to enhance immunogenicity, it is widely appreciated that fusion proteins can also facilitate the expression of proteins, and, accordingly, can be used in the expression of the polypeptides of the present invention (see, for example, *Current Protocols in Molecular Biology*, eds. Ausubel *et al.* (N.Y.: John Wiley & Sons, 1991)). In another embodiment, a fusion gene coding for a purification leader sequence, such as a poly-(His)/enterokinase cleavage site sequence at the N-terminus of the desired portion of the recombinant protein, can allow purification of the expressed fusion protein by affinity chromatography using a Ni²⁺ metal resin. The purification leader sequence can then be subsequently removed by treatment with enterokinase to provide the purified protein (e.g., see Hochuli *et al.* (1987) *J. Chromatography* 411:177; and Janknecht *et al.* *PNAS* 88:8972).

Techniques for making fusion genes are known to those skilled in the art. Essentially, the joining of various DNA fragments coding for different polypeptide sequences is performed in accordance with conventional techniques, employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of nucleic acid fragments can be carried out using anchor primers which give rise to complementary overhangs between two consecutive nucleic acid fragments which can subsequently be annealed to generate a chimeric nucleic acid sequence (see, for example, *Current Protocols in Molecular Biology*, eds. Ausubel *et al.* John Wiley & Sons: 1992).

The present invention further pertains to methods of producing the subject polypeptides. For example, a host cell transfected with a nucleic acid vector directing

expression of a nucleotide sequence encoding the subject polypeptides can be cultured under appropriate conditions to allow expression of the peptide to occur. Suitable media for cell culture are well known in the art. The recombinant polypeptide can be isolated from cell culture medium, host cells, or both using techniques known in the art for purifying proteins including ion-exchange chromatography, gel filtration chromatography, ultrafiltration, electrophoresis, and immunoaffinity purification with antibodies specific for such peptide. In a preferred embodiment, the recombinant polypeptide is a fusion protein containing a domain which facilitates its purification, such as GST fusion protein.

Moreover, it will be generally appreciated that, under certain circumstances, it may be advantageous to provide homologs of one of the subject polypeptides which function in a limited capacity as one of either an agonist (mimetic) or an antagonist, in order to promote or inhibit only a subset of the biological activities of the naturally occurring form of the protein. Thus, specific biological effects can be elicited by treatment with a homolog of limited function, and with fewer side effects relative to treatment with agonists or antagonists which are directed to all of the biological activities of naturally occurring forms of subject proteins.

Homologs of each of the subject polypeptide can be generated by mutagenesis, such as by discrete point mutation(s), or by truncation. For instance, mutation can give rise to homologs which retain substantially the same, or merely a subset, of the biological activity of the polypeptide from which it was derived. Alternatively, antagonistic forms of the polypeptide can be generated which are able to inhibit the function of the naturally occurring form of the protein, such as by competitively binding to a receptor.

The recombinant polypeptides of the present invention also include homologs of the wild-type proteins, such as versions of those proteins which are resistant to proteolytic cleavage, for example, due to mutations which alter ubiquitination or other enzymatic targeting associated with the protein.

Polypeptides may also be chemically modified to create derivatives by forming covalent or aggregate conjugates with other chemical moieties, such as glycosyl groups, lipids, phosphate, acetyl groups and the like. Covalent derivatives of proteins can be prepared by linking the chemical moieties to functional groups on

amino acid sidechains of the protein or at the N-terminus or at the C-terminus of the polypeptide.

Modification of the structure of the subject polypeptides can be for such purposes as enhancing therapeutic or prophylactic efficacy, stability (e.g., *ex vivo* shelf life and resistance to proteolytic degradation), or post-translational modifications (e.g., to alter phosphorylation pattern of protein). Such modified peptides, when designed to retain at least one activity of the naturally occurring form of the protein, or to produce specific antagonists thereof, are considered functional equivalents of the polypeptides described in more detail herein. Such modified peptides can be produced, for instance, by amino acid substitution, deletion, or addition. The substitutional variant may be a substituted conserved amino acid or a substituted non-conserved amino acid.

For example, it is reasonable to expect that an isolated replacement of a leucine with an isoleucine or valine, an aspartate with a glutamate, a threonine with a serine, or a similar replacement of an amino acid with a structurally related amino acid (i.e., isosteric and/or isoelectric mutations) will not have a major effect on the biological activity of the resulting molecule. Conservative replacements are those that take place within a family of amino acids that are related in their side chains.

Genetically encoded amino acids can be divided into four families: (1) acidic = aspartate, glutamate; (2) basic = lysine, arginine, histidine; (3) nonpolar = alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan; and (4) uncharged polar = glycine, asparagine, glutamine, cysteine, serine, threonine, tyrosine. In similar fashion, the amino acid repertoire can be grouped as (1) acidic = aspartate, glutamate; (2) basic = lysine, arginine, histidine; (3) aliphatic = glycine, alanine, valine, leucine, isoleucine, serine, threonine, with serine and threonine optionally be grouped separately as aliphatic-hydroxyl; (4) aromatic = phenylalanine, tyrosine, tryptophan; (5) amide = asparagine, glutamine; and (6) sulfur-containing = cysteine and methionine. (see, for example, Biochemistry, 2nd ed., Ed. by L. Stryer, WH Freeman and Co.: 1981). Whether a change in the amino acid sequence of a peptide results in a functional homolog (e.g., functional in the sense that the resulting polypeptide mimics or antagonizes the wild-type form) can be readily determined by assessing the ability of the variant peptide to produce a response in cells in a fashion similar to the wild-type protein, or competitively inhibit such a response.

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Polypeptides in which more than one replacement has taken place can readily be tested in the same manner. The variant may be designed so as to retain biological activity of a particular region of the protein. In a non-limiting example, Osawa et al., 1994, Biochemistry and Molecular International 34:1003-1009, discusses the actin binding region of a protein from several different species. The actin binding regions of these species are considered homologous based on the fact that they have amino acids that fall within "homologous residue groups." Homologous residues are judged according to the following groups (using single letter amino acid designations): STAG; ILVMF; HRK; DEQN; and FYW. For example, an S, a T, an A or a G can be in a position and the function (in this case actin binding) is retained.

Additional guidance on amino acid substitution is available from studies of protein evolution. Go et al., 1980, Int. J. Peptide Protein Res. 15:211-224, classified amino acid residue sites as interior or exterior depending on their accessibility. More frequent substitution on exterior sites was confirmed to be general in eight sets of homologous protein families regardless of their biological functions and the presence or absence of a prosthetic group. Virtually all types of amino acid residues had higher mutabilities on the exterior than in the interior. No correlation between mutability and polarity was observed of amino acid residues in the interior and exterior, respectively. Amino acid residues were classified into one of three groups depending on their polarity: polar (Arg, Lys, His, Gln, Asn, Asp, and Glu); weak polar (Ala, Pro, Gly, Thr, and Ser), and nonpolar (Cys, Val, Met, Ile, Leu, Phe, Tyr, and Trp). Amino acid replacements during protein evolution were very conservative: 88% and 76% of them in the interior or exterior, respectively, were within the same group of the three. Inter-group replacements are such that weak polar residues are replaced more often by nonpolar residues in the interior and more often by polar residues on the exterior.

Querol et al., 1996, Prot. Eng. 9:265-271, provides general rules for amino acid substitutions to enhance protein thermostability. New glycosylation sites can be introduced as discussed in Olsen and Thomsen, 1991, J. Gen. Microbiol. 137:579-585. An additional disulfide bridge can be introduced, as discussed by Perry and Wetzel, 1984, Science 226:555-557; Pantoliano et al., 1987, Biochemistry 26:2077-2082; Matsumura et al., 1989, Nature 342:291-293; Nishikawa et al., 1990, Protein Eng. 3:443-448; Takagi et al., 1990, J. Biol. Chem. 265:6874-6878; Clarke et al., 1993, Biochemistry 32:4322-4329; and Wakarchuk et al., 1994, Protein Eng. 7:1379-1386.

An additional metal binding site can be introduced, according to Toma *et al.*, 1991, *Biochemistry* 30:97-106, and Haezebrouck *et al.*, 1993, *Protein Eng.* 6:643-649. Substitutions with prolines in loops can be made according to Másul *et al.*, 1994, *Appl. Env. Microbiol.* 60:3579-3584; and Hardy *et al.*, *FEBS Lett.* 317:89-92.

5 Cysteine-depleted muteins are considered variants within the scope of the invention. These variants can be constructed according to methods disclosed in U.S. Patent No. 4,959,314, which discloses how to substitute other amino acids for cysteines, and how to determine biological activity and effect of the substitution. Such methods are suitable for proteins according to this invention that have cysteine
10 residues suitable for such substitutions, for example to eliminate disulfide bond formation.

To learn the identity and function of the gene that correlates with an nucleic acid, the nucleic acids or corresponding amino acid sequences can be screened against profiles of protein families. Such profiles focus on common structural motifs among
15 proteins of each family. Publicly available profiles are described above. Additional or alternative profiles are described below.

In comparing a new nucleic acid with known sequences, several alignment tools are available. Examples include PileUp, which creates a multiple sequence alignment, and is described in Feng *et al.*, *J. Mol. Evol.* (1987) 25:351-360. Another
20 method, GAP, uses the alignment method of Needleman *et al.*, *J. Mol. Biol.* (1970) 48:443-453. GAP is best suited for global alignment of sequences. A third method, BestFit, functions by inserting gaps to maximize the number of matches using the local homology algorithm of Smith and Waterman, *Adv. Appl. Math.* (1981) 2:482-489.

25 Examples of such profiles are described below.

Chemokines

Chemokines are a family of proteins that have been implicated in lymphocyte trafficking, inflammatory diseases, angiogenesis, hematopoiesis, and viral infection.
30 See, for example, Rollins, *Blood* (1997) 90(3):909-928, and Wells *et al.*, *J. Leuk. Biol.* (1997) 61:545-550. U.S. Patent No. 5,605,817 discloses DNA encoding a chemokine expressed in fetal spleen. U.S. Patent No. 5,656,724 discloses chemokine-like

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proteins and methods of use. U.S. Patent No. 5,602,008 discloses DNA encoding a chemokine expressed by liver.

Mutants of the encoded chemokines are polypeptides having an amino acid sequence that possesses at least one amino acid substitution, addition, or deletion as compared to native chemokines. Fragments possess the same amino acid sequence of the native chemokines; mutants may lack the amino and/or carboxyl terminal sequences. Fusions are mutants, fragments, or the native chemokines that also include amino and/or carboxyl terminal amino acid extensions.

The number or type of the amino acid changes is not critical, nor is the length or number of the amino acid deletions, or amino acid extensions that are incorporated in the chemokines as compared to the native chemokine amino acid sequences. A polynucleotide encoding one of these variant polypeptides will retain at least about 80% amino acid identity with at least one known chemokine. Preferably, these polypeptides will retain at least about 85% amino acid sequence identity, more preferably, at least about 90%; even more preferably, at least about 95%. In addition, the variants will exhibit at least 80%; preferably about 90%; more preferably about 95% of at least one activity exhibited by a native chemokine. Chemokine activity includes immunological, biological, receptor binding, and signal transduction functions of the native chemokine.

Chemotaxis. Assays for chemotaxis relating to neutrophils are described in Walz *et al.*, *Biochem. Biophys. Res. Commun.* (1987) 149:755, Yoshimura *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1987) 84:9233, and Schroder *et al.*, *J. Immunol.* (1987) 139:3474; to lymphocytes, Larsen *et al.*, *Science* (1989) 243:1464, Carr *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1994) 91:3652; to tumor-infiltrating lymphocytes, Liao *et al.*, *J. Exp. Med.* (1995) 182:1301; to hemopoietic progenitors, Aiuti *et al.*, *J. Exp. Med.* (1997) 185:111; to monocytes, Valente *et al.*, *Biochem.* (1988) 27:4162; and to natural killer cells, Loetscher *et al.*, *J. Immunol.* (1996) 156:322, and Allavena *et al.*, *Eur. J. Immunol.* (1994) 24:3233.

Assays for determining the biological activity of attracting eosinophils are described in Dahinden *et al.*, *J. Exp. Med.* (1994) 179:751, Weber *et al.*, *J. Immunol.* (1995) 154:4166, and Noso *et al.*, *Biochem. Biophys. Res. Commun.* (1994) 200:1470; for attracting dendritic cells, Sozzani *et al.*, *J. Immunol.* (1995) 155:3292; for attracting basophils, in Dahinden *et al.*, *J. Exp. Med.* (1994) 179:751, Alam *et al.*, *J.*

5 Receptor Binding. Native chemokines exhibit binding activity with a number
of receptors. Description of such receptors and assays to detect binding are described
in, for example, Murphy *et al.*, *Science* (1991) 253:1280; Combadiere *et al.*, *J. Biol.*
Chem. (1995) 270:29671; Daugherty *et al.*, *J. Exp. Med.* (1996) 183:2349; Samson *et*
al., *Biochem.* (1996) 35:3362; Raport *et al.*, *J. Biol. Chem.* (1996) 271:17161;
10 Combadiere *et al.*, *J. Leukoc. Biol.* (1996) 60:147; Baba *et al.*, *J. Biol. Chem.* (1997)
23:14893; Yosida *et al.*, *J. Biol. Chem.* (1997) 272:13803; Arvanitakis *et al.*, *Nature*
(1997) 385:347, and many other assays are known in the art.

Glycosaminoglycan production can be induced by native chemokines, assayed as described in Castor *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1983) 80:765. Chemokine-mediated histamine release from basophils is assayed as described in Dahinden *et al.*, *J. Exp. Med.* (1989) 170:1787; and White *et al.*, *Immunol. Lett.* (1989) 22:151. Heparin binding is described in Luster *et al.*, *J. Exp. Med.* (1995) 182:219.

Dimerization Activity. Chemokines can possess dimerization activity, which can be assayed according to Burrows *et al.*, *Biochem.* (1994) 33:12741; and Zhang *et al.*, *Mol. Cell. Biol.* (1995) 15:4851. Native chemokines can play a role in the inflammatory response of viruses. This activity can be assayed as described in Bleul *et al.*, *Nature* (1996) 382:829; and Oberlin *et al.*, *Nature* (1996) 382:833. Exocytosis of monocytes can be promoted by native chemokines. The assay for such activity is described in Uguccioni *et al.*, *Eur. J. Immunol.* (1995) 25:64. Native chemokines also can inhibit hemapoietic stem cell proliferation. The method for testing for such activity is reported in Graham *et al.*, *Nature* (1990) 344:442.

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Ihle, *Cell* (1995) 81:479-482, Pan *et al*, *Science* (1997) 276:111-113, Duan and Dixit, *Nature* (1997) 385:86-89, and Chinnaiyan *et al*, *Science* (1996) 274:990-992). U.S. Patent No. 5,563,039 describes a protein homologous to TRADD (Tumor Necrosis Factor Receptor-1 Associated Death Domain containing protein), and modifications of
5 the active domain of TRADD that retain the functional characteristics of the protein, as well as apoptosis assays for testing the function of such death domain containing proteins. U.S. Patent No. 5,658,883 discloses biologically active TGF-B1 peptides. U.S. Patent No. 5,674,734 discloses protein RIP which contains a C-terminal death domain and an N-terminal kinase domain.

- 10 Leukemia Inhibitory Factor (LIF) An LIF profile is constructed from sequences of leukemia inhibitor factor, CT-1 (cardiotrophin-1), CNTF (ciliary neurotrophic factor), OSM (oncostatin M), and IL-6 (interleukin-6). This profile encompasses a family of secreted cytokines that have pleiotropic effects on many cell types including hepatocytes, osteoclasts, neuronal cells and cardiac myocytes, and can
15 be used to detect additional genes encoding such proteins. These molecules are all structurally related and share a common co-receptor gp130 which mediates intracellular signal transduction by cytoplasmic tyrosine kinases such as src.

- Novel proteins related to this family are also likely to be secreted, to activate gp130 and to function in the development of a variety of cell types. Thus new
20 members of this family would be candidates to be developed as growth or survival factors for the cell types that they stimulate. For more details on this family of cytokines, see Pennica *et al*, *Cytokine and Growth Factor Reviews* (1996) 7:81-91. U.S. Patent No. 5,420,247 discloses LIF receptor and fusion proteins. U.S. Patent No. 5,443,825 discloses human LIF.

- 25 Angiopoietin Angiopoietin-1 is a secreted ligand of the TIE-2 tyrosine kinase; it functions as an angiogenic factor critical for normal vascular development. Angiopoietin-2 is a natural antagonist of angiopoietin-1 and thus functions as an anti-angiogenic factor. These two proteins are structurally similar and activate the same receptor. (Folkman and D'Amore, *Cell* (1996) 87:1153-1155, and Davis *et al.*, *Cell*
30 (1996) 87:1161-1169.)

The angiopoietin molecules are composed of two domains, a coiled-coil region and a region related to fibrinogen. The fibrinogen domain is found in many molecules including ficolin and tesascin, and is well defined structurally with many members.

Receptor Protein-Tyrosine Kinases Receptor Protein-Tyrosine Kinases or RPTKs are described in Lindberg, *Annu. Rev. Cell Biol.* (1994) 10:251-337.

Growth Factors: Epidermal Growth Factor (EGF) and Fibroblast Growth Factor (FGF)

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For a discussion of growth factor superfamilies, see Growth Factors: A Practical Approach, Appendix A1 (Ed. McKay and Leigh, Oxford University Press, NY, 1993) pp. 237-243.

The alignments (pretty box) for EGF and FGF are shown in Figures 1 and 2, respectively. U.S. Patent No. 4,444,760 discloses acidic brain fibroblast growth factor, which is active in the promotion of cell division and wound healing. U.S. Patent No. 5,439,818 discloses DNA encoding human recombinant basic fibroblast growth factor, which is active in wound healing. U.S. Patent No. 5,604,293 discloses recombinant human basic fibroblast growth factor, which is useful for wound healing. U.S. Patent No. 5,410,832 discloses brain-derived and recombinant acidic fibroblast growth factor, which act as mitogens for mesoderm and neuroectoderm-derived cells in culture, and promote wound healing in soft tissue, cartilaginous tissue and musculo-skeletal tissue. U.S. Patent No. 5,387,673 discloses biologically active fragments of FGF that retain activity.

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Proteins of the TNF Family A profile derived from the TNF family is created by aligning sequences of the following TNF family members: nerve growth factor (NGF), lymphotoxin, Fas ligand, tumor necrosis factor (TNF), CD40 ligand, TRAIL, ox40 ligand, 4-1BB ligand, CD27 ligand, and CD30 ligand. The profile is designed to identify sequences of proteins that constitute new members or homologues of this family of proteins.

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U.S. Patent No. 5,606,023 discloses mutant TNF proteins; U.S. Patent No. 5,597,899 and U.S. Patent No. 5,486,463 disclose TNF muteins; and U.S. Patent No. 5,652,353 discloses DNA encoding TNF- α muteins.

Members of the TNF family of proteins have been shown in vitro to multimerize, as described in Burrows *et al.*, *Biochem.* (1994) 33:12741 and Zhang *et al.*, *Mol. Cell. Biol.* (1995) 15:4851 and bind receptors as described in Browning *et al.*, *J. Immunol.* (1994) 147:1230, Androlewicz *et al.*, *J. Biol. Chem.* (1992) 267:2542, and Crowe *et al.*, *Science* (1994) 264:707.

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In vivo, TNFs proteolytically cleave a target protein as described in Kriegel *et al.*, *Cell* (1988) 53:45 and Mohler *et al.*, *Nature* (1994) 370:218 and demonstrate cell proliferation and differentiation activity. T-cell or thymocyte proliferation is assayed as described in Armitage *et al.*, *Eur. J. Immunol.* (1992) 22:447; Current Protocols in Immunology, ed. J.E. Coligan *et al.*, 3.1-3.19; Takai *et al.*, *J. Immunol.* (1986) 137:3494-3500, Bertagnoli *et al.*, *J. Immunol.* (1990) 145:1706-1712, Bertagnoli *et al.*, *J. Immunol.* (1991) 133:327-340, Bertagnoli *et al.*, *J. Immunol.* (1992) 149:3778-3783, and Bowman *et al.*, *J. Immunol.* (1994) 152:1756-1761. B cell proliferation and Ig secretion are assayed as described in Maliszewski, *J. Immunol.* (1990) 144:3028-3033, and Assays for B Cell Function: In vitro antibody production, Mond and Brunswick, Current Protocols in Immunol., Coligan Ed vol 1 pp 3.8.1-3.8.16, John Wiley and Sons, Toronto 1994, Kehrl *et al.*, *Science* (1987) 238:1144 and Boussiotis *et al.*, *PNAS USA* (1994) 91:7067.

Other in vivo activities include upregulation of cell surface antigens, upregulation of costimulatory molecules, and cellular aggregation/adhesion as described in Barrett *et al.*, *J. Immunol.* (1991) 146:1722; Bjorck *et al.*, *Eur. J. Immunol.* (1993) 23:1771; Clark *et al.*, *Annu Rev. Immunol.* (1991) 9:97; Ranheim *et al.*, *J. Exp. Med.* (1994) 177:925; Yellin, *J. Immunol.* (1994) 153:666; and Gruss *et al.*, *Blood* (1994) 84:2305.

Proliferation and differentiation of hematopoietic and lymphopoietic cells has also been shown in vivo for TNFs, using assays for embryonic differentiation and hematopoiesis as described in Johansson *et al.*, *Cellular Biology* (1995) 15:141-151, Keller *et al.*, *Mol. Cell. Biol.* (1993) 13:473-486, McClanahan *et al.*, *Blood* (1993) 81:2903-2915 and using assays to detect stem cell survival and differentiation as described in Culture of Hematopoietic Cells, Freshney *et al.* eds, pp 1-21, 27-29, 139-162, 163-179, and 265-268, Wiley-Liss, Inc., New York, NY, 1994, and Hirajama *et al.*, *PNAS USA* (1992) 89:5907-5911.

In vivo activities of TNFs also include lymphocyte survival and apoptosis, assayed as described in Darzynkewicz *et al.*, *Cytometry* (1992) 13:795-808; Gorczyca *et al.*, *Leukemia* (1993) 7:659-670; Itoh *et al.*, *Cell* (1991) 66:233-243; Zacharduk, *J. Immunol.* (1990) 145:4037-4045; Zamai *et al.*, *Cytometry* (1993) 14:891-897; and Gorczyca *et al.*, *Int'l J. Oncol.* (1992) 1:639-648.

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Some members of the TNF family are cleaved from the cell surface; others remain membrane bound. The three-dimensional structure of TNF is discussed in Sprang and Eck, Tumor Necrosis Factors; *supra*.

TNF proteins include a transmembrane domain. The protein is cleaved into a shorter soluble version, as described in Kriegler *et al.*, *Cell* (1988) 53:45-53, Perez *et al.*, *Cell* (1990) 63:251-258, and Shaw *et al.*, *Cell* (1986) 46:659-667. The transmembrane domain is between amino acid 46 and 77 and the cytoplasmic domain is between position 1 and 45 on the human form of TNF α . The 3-dimensional motifs of TNF include a sandwich of two pleated β -sheets. Each sheet is composed of anti-parallel α -strands. α -Strands facing each other on opposite sites of the sandwich are connected by short polypeptide loops, as described in Van Ostade *et al.*, *Protein Engineering* (1994) 7(1):5-22, and Sprang *et al.*, Tumor Necrosis Factors; *supra*.

Residues of the TNF family proteins that are involved in the β -sheet secondary structure have been identified as described in Van Ostade *et al.*, *Protein Engineering* (1994) 7(1):5-22, and Sprang *et al.*, Tumor Necrosis Factors; *supra*.

TNF receptors are disclosed in U.S. Patent No. 5,395,760. A profile derived from the TNF receptor family is created by aligning sequences of the TNF receptor family, including Apo1/Fas, TNFR I and II, death receptor3 (DR3), CD40, ox40, CD27, and CD30. Thus, the profile is designed to identify, from the nucleic acids of the invention, sequences of proteins that constitute new members or homologs of this family of proteins.

Tumor necrosis factor receptors exist in two forms in humans: p55 TNFR and p75 TNFR, both of which provide intracellular signals upon binding with a ligand. The extracellular domains of these receptor proteins are cysteine rich. The receptors can remain membrane bound, although some forms of the receptors are cleaved forming soluble receptors. The regulation, diagnostic, prognostic, and therapeutic value of soluble TNF receptors is discussed in Aderka, *Cytokine and Growth Factor Reviews*, (1996) 7(3):231-240.

PDGF Family U.S. Patent No. 5,326,695 discloses platelet derived growth factor agonists; bioactive portions of PDGF-B are used as agonists. U.S. Patent No. 4,845,075 discloses biologically active B-chain homodimers, and also includes variants and derivatives of the PDGF-B chain. U.S. Patent No. 5,128,321 discloses

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PDGF analogs and methods of use. Proteins having the same bioactivity as PDGF are disclosed, including A and B chain proteins.

Kinase (Including MKK) Family U.S. Patent No. 5,650,501 discloses serine/threonine kinase, associated with mitotic and meiotic cell division; the protein
5 has a kinase domain in its N-terminal and 3 PEST regions in the C-terminus. U.S. Patent No. 5,605,825 discloses human PAK65, a serine protein kinase.

The foregoing discussion provides a few examples of the protein profiles that can be compared with the nucleic acids of the invention. One skilled in the art can use these and other protein profiles to identify the genes that correlate with the nucleic
10 acids.

IX. Determining the Function of the Encoded Expression Products

Ribozymes, antisense constructs, dominant negative mutants, and triplex formation can be used to determine function of the expression product of an nucleic
15 acid-related gene.

A. Ribozymes

Trans-cleaving catalytic RNAs (ribozymes) are RNA molecules possessing endoribonuclease activity. Ribozymes are specifically designed for a particular target, and the target message must contain a specific nucleotide sequence. They are
20 engineered to cleave any RNA species site-specifically in the background of cellular RNA. The cleavage event renders the mRNA unstable and prevents protein expression. Importantly, ribozymes can be used to inhibit expression of a gene of unknown function for the purpose of determining its function in an in vitro or in vivo context, by detecting the phenotypic effect.

25 One commonly used ribozyme motif is the hammerhead, for which the substrate sequence requirements are minimal. Design of the hammerhead ribozyme is disclosed in Usman *et al.*, *Current Opin. Struct. Biol.* (1996) 6:527-533. Usman also discusses the therapeutic uses of ribozymes. Ribozymes can also be prepared and used as described in Long *et al.*, *FASEB J.* (1993) 7:25; Symons, *Ann. Rev. Biochem.* (1992) 61:641; Perrotta *et al.*, *Biochem.* (1992) 31:16-17; Ojwang *et al.*,
30 *Proc. Natl. Acad. Sci. (USA)* (1992) 89:10802-10806; and U.S. Patent No. 5,254,678. Ribozyme cleavage of HIV-I RNA is described in U.S. Patent No. 5,144,019; methods of cleaving RNA using ribozymes is described in U.S. Patent No.

5,116,742; and methods for increasing the specificity of ribozymes are described in U.S. Patent No. 5,225,337 and Koizumi *et al.*, *Nucleic Acid Res.* (1989) 17:7059-7071. Preparation and use of ribozyme fragments in a hammerhead structure are also described by Koizumi *et al.*, *Nucleic Acids Res.* (1989) 17:7059-7071. Preparation
5 and use of ribozyme fragments in a hairpin structure are described by Chowrira and Burke, *Nucleic Acids Res.* (1992) 20:2835. Ribozymes can also be made by rolling transcription as described in Daubendiek and Kool, *Nat. Biotechnol.* (1997) 15(3):273-277.

The hybridizing region of the ribozyme may be modified or may be prepared
10 as a branched structure as described in Horn and Urdea, *Nucleic Acids Res.* (1989) 17:6959-67. The basic structure of the ribozymes may also be chemically altered in ways familiar to those skilled in the art, and chemically synthesized ribozymes can be administered as synthetic oligonucleotide derivatives modified by monomeric units. In a therapeutic context, liposome mediated delivery of ribozymes improves cellular
15 uptake, as described in Birikh *et al.*, *Eur. J. Biochem.* (1997) 245:1-16.

Using the nucleic acid sequences of the invention and methods known in the art, ribozymes are designed to specifically bind and cut the corresponding mRNA species. Ribozymes thus provide a means to inhibit the expression of any of the proteins encoded by the disclosed nucleic acids or their full-length genes. The full-
20 length gene need not be known in order to design and use specific inhibitory ribozymes. In the case of a nucleic acid or cDNA of unknown function, ribozymes corresponding to that nucleotide sequence can be tested in vitro for efficacy in cleaving the target transcript. Those ribozymes that effect cleavage in vitro are further tested in vivo. The ribozyme can also be used to generate an animal model for a
25 disease, as described in Birikh *et al.*, *Eur. J. Biochem.* (1997) 245:1-16. An effective ribozyme is used to determine the function of the gene of interest by blocking its transcription and detecting a change in the cell. Where the gene is found to be a mediator in a disease, an effective ribozyme is designed and delivered in a gene therapy for blocking transcription and expression of the gene.

30 Therapeutic and functional genomic applications of ribozymes proceed beginning with knowledge of a portion of the coding sequence of the gene to be inhibited. Thus, for many genes, a partial nucleic acid sequence provides adequate sequence for constructing an effective ribozyme. A target cleavage site is selected in

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B. Antisense

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Drug Design (1997) 12:327-339); and protein kinase C (McGraw *et al.*, *Anti-Cancer Drug Design* (1997) 12:315-326.

Given the extensive background literature and clinical experience in antisense therapy, one skilled in the art can use selected nucleic acids of the invention as
5 additional potential therapeutics. The choice of nucleic acid can be narrowed by first testing them for binding to "hot spot" regions of the genome of cancerous cells. If a nucleic acid is identified as binding to a "hot spot", testing the nucleic acid as an antisense compound in the corresponding cancer cells clearly is warranted.

Ogunbiyi *et al.*, *Gastroenterology* (1997) 113(3):761-766 describe prognostic
10 use of allelic loss in colon cancer; Barks *et al.*, *Genes, Chromosomes, and Cancer* (1997) 19(4):278-285 describe increased chromosome copy number detected by FISH in malignant melanoma; Nishizake *et al.*, *Genes, Chromosomes, and Cancer* (1997) 19(4):267-272 describe genetic alterations in primary breast cancer and their metastases and direct comparison using modified comparative genome hybridization;
15 and Elo *et al.*, *Cancer Research* (1997) 57(16):3356-3359 disclose that loss of heterozygosity at 16z24.1-q24.2 is significantly associated with metastatic and aggressive behavior of prostate cancer.

C. Dominant Negative Mutations

20 As an alternative method for identifying function of the nucleic acid-related gene, dominant negative mutations are readily generated for corresponding proteins that are active as homomultimers. A mutant polypeptide will interact with wild-type polypeptides (made from the other allele) and form a non-functional multimer. Thus, a mutation is in a substrate-binding domain, a catalytic domain, or a cellular
25 localization domain. Preferably, the mutant polypeptide will be overproduced. Point mutations are made that have such an effect. In addition, fusion of different polypeptides of various lengths to the terminus of a protein can yield dominant negative mutants. General strategies are available for making dominant negative mutants. See Herskowitz, *Nature* (1987) 329:219-222. Such a technique can be used
30 for creating a loss-of-function mutation, which is useful for determining the function of a protein.

D. Triplex Formation

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Endogenous gene expression can also be reduced by inactivating or “knocking out” the gene or its promoter using targeted homologous recombination. (E.g., see Smithies *et al.*, 1985, Nature 317:230-234; Thomas & Capecchi, 1987, Cell 51:503-512; Thompson *et al.*, 1989 Cell 5:313-321; each of which is incorporated by
5 reference herein in its entirety). For example, a mutant, non-functional gene (or a completely unrelated DNA sequence) flanked by DNA homologous to the endogenous gene (either the coding regions or regulatory regions of the gene) can be used, with or without a selectable marker and/or a negative selectable marker, to transfect cells that express that gene *in vivo*. Insertion of the DNA construct, via
10 targeted homologous recombination, results in inactivation of the gene.

Alternatively, endogenous gene expression can be reduced by targeting deoxyribonucleotide sequences complementary to the regulatory region of the target gene (i.e., the gene promoter and/or enhancers) to form triple helical structures that prevent transcription of the gene in target cells in the body. (See generally, Helene, C.
15 1991, Anticancer Drug Des., 6(6):569-84; Helene, C., *et al.*, 1992, Ann. N.Y. Acad. Sci., 660:27-36; and Maher, L.J., 1992, Bioassays 14(12):807-15).

Nucleic acid molecules to be used in triple helix formation for the inhibition of transcription are preferably single stranded and composed of deoxyribonucleotides. The base composition of these oligonucleotides should promote triple helix formation
20 via Hoogsteen base-pairing rules, which generally require sizable stretches of either purines or pyrimidines to be present on one strand of a duplex. Nucleotide sequences may be pyrimidine-based, which will result in TAT and CGC triplets across the three associated strands of the resulting triple helix. The pyrimidine-rich molecules provide base complementarity to a purine-rich region of a single strand of the duplex in a
25 parallel orientation to that strand. In addition, nucleic acid molecules may be chosen that are purine-rich, for example, containing a stretch of G residues. These molecules will form a triple helix with a DNA duplex that is rich in GC pairs, in which the majority of the purine residues are located on a single strand of the targeted duplex, resulting in CGC triplets across the three strands in the triplex.

30 Alternatively, the potential sequences that can be targeted for triple helix formation may be increased by creating a so called “switchback” nucleic acid molecule. Switchback molecules are synthesized in an alternating 5'-3', 3'-5' manner, such that they base pair with first one strand of a duplex and then the other,

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eliminating the necessity for a sizable stretch of either purines or pyrimidines to be present on one strand of a duplex.

Antisense RNA and DNA, ribozyme, and triple helix molecules of the invention may be prepared by any method known in the art for the synthesis of DNA and RNA molecules. These include techniques for chemically synthesizing oligodeoxyribonucleotides and oligoribonucleotides well known in the art such as for example solid phase phosphoramidite chemical synthesis. Alternatively, RNA molecules may be generated by *in vitro* and *in vivo* transcription of DNA sequences encoding the antisense RNA molecule. Such DNA sequences may be incorporated into a wide variety of vectors which incorporate suitable RNA polymerase promoters such as the T7 or SP6 polymerase promoters. Alternatively, antisense cDNA constructs that synthesize antisense RNA constitutively or inducibly, depending on the promoter used, can be introduced stably into cell lines.

Moreover, various well known modifications to nucleic acid molecules may be introduced as a means of increasing intracellular stability and half-life. Possible modifications include but are not limited to the addition of flanking sequences of ribonucleotides or deoxyribonucleotides to the 5' and/or 3' ends of the molecule or the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages within the oligodeoxyribonucleotide backbone.

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X. Diagnostic & Prognostic Assays and Drug Screening Methods

The present invention provides method for determining whether a subject is at risk for developing a disease or condition characterized by unwanted cell proliferation by detecting the disclosed biomarkers, i.e., the disclosed nucleic acid markers (SEQ ID Nos: 1-544) and/or polypeptide markers for colon cancer encoded thereby.

In clinical applications, human tissue samples can be screened for the presence and/or absence of the biomarkers identified herein. Such samples could consist of needle biopsy cores, surgical resection samples, lymph node tissue, or serum. For example, these methods include obtaining a biopsy, which is optionally fractionated by cryostat sectioning to enrich tumor cells to about 80% of the total cell population. In certain embodiments, nucleic acids extracted from these samples may be amplified using techniques well known in the art. The levels of selected markers detected

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would be compared with statistically valid groups of metastatic, non-metastatic malignant, benign, or normal colon tissue samples.

In one embodiment, the diagnostic method comprises determining whether a subject has an abnormal mRNA and/or protein level of the disclosed markers, such as
5 by Northern blot analysis, reverse transcription-polymerase chain reaction (RT-PCR),
in situ hybridization, immunoprecipitation, Western blot hybridization, or immunohistochemistry. According to the method, cells are obtained from a subject and the levels of the disclosed biomarkers, protein or mRNA level, is determined and compared to the level of these markers in a healthy subject. An abnormal level of the
10 biomarker polypeptide or mRNA levels is likely to be indicative of cancer such as colon cancer.

Accordingly, in one aspect, the invention provides probes and primers that are specific to the unique nucleic acid markers disclosed herein. Accordingly, the nucleic acid probes comprise a nucleotide sequence at least 12 nucleotides in length,
15 preferably at least 15 nucleotides, more preferably, 25 nucleotides, and most preferably at least 40 nucleotides, and up to all or nearly all of the coding sequence which is complementary to a portion of the coding sequence of a marker nucleic acid sequence, which nucleic acid sequence is represented by SEQ ID Nos: 1-544 or a sequence complementary thereto.

20 In one embodiment, the method comprises using a nucleic acid probe to determine the presence of cancerous cells in a tissue from a patient. Specifically, the method comprises:

1. providing a nucleic acid probe comprising a nucleotide
sequence at least 12 nucleotides in length, preferably at least 15
25 nucleotides, more preferably, 25 nucleotides, and most preferably at least 40 nucleotides, and up to all or nearly all of the coding sequence which is complementary to a portion of the coding sequence of a nucleic acid sequence represented by SEQ ID Nos: 1-544 or a sequence complementary thereto and is
30 differentially expressed in tumors cells, such as colon cancer cells;
2. obtaining a tissue sample from a patient potentially comprising cancerous cells;

3. providing a second tissue sample containing cells substantially all of which are non-cancerous;
4. contacting the nucleic acid probe under stringent conditions with RNA of each of said first and second tissue samples (e.g., in a Northern blot or in situ hybridization assay); and
5. comparing (a) the amount of hybridization of the probe with RNA of the first tissue sample, with (b) the amount of hybridization of the probe with RNA of the second tissue sample; wherein a statistically significant difference in the amount of hybridization with the RNA of the first tissue sample as compared to the amount of hybridization with the RNA of the second tissue sample is indicative of the presence of cancerous cells in the first tissue sample.

In one aspect, the method comprises in situ hybridization with a probe derived from a given marker nucleic acid sequence, which nucleic acid sequence is represented by SEQ ID Nos: 1-544 or a sequence complementary thereto. The method comprises contacting the labeled hybridization probe with a sample of a given type of tissue potentially containing cancerous or pre-cancerous cells as well as normal cells, and determining whether the probe labels some cells of the given tissue type to a degree significantly different (e.g., by at least a factor of two, or at least a factor of five, or at least a factor of twenty, or at least a factor of fifty) than the degree to which it labels other cells of the same tissue type.

Also within the invention is a method of determining the phenotype of a test cell from a given human tissue, e.g., whether the cell is (a) normal, or (b) cancerous or precancerous, by contacting the mRNA of a test cell with a nucleic acid probe at least 12 nucleotides in length, preferably at least 15 nucleotides, more preferably at least 25 nucleotides, and most preferably at least 40 nucleotides, and up to all or nearly all of a sequence which is complementary to a portion of the coding sequence of a nucleic acid sequence represented by SEQ ID Nos: 1-544 or a sequence complementary thereto, and which is differentially expressed in tumor cells as compared to normal cells of the given tissue type; and determining the approximate amount of hybridization of the probe to the mRNA, an amount of hybridization either more or less than that seen with the mRNA of a normal cell of that tissue type being indicative that the test cell is cancerous or pre-cancerous.

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Alternatively, the above diagnostic assays may be carried out using antibodies to detect the protein product encoded by the marker nucleic acid sequence, which nucleic acid sequence is represented by SEQ ID Nos: 1-544 or a sequence complementary thereto. Accordingly, in one embodiment, the assay would include
5 contacting the proteins of the test cell with an antibody specific for the gene product of a nucleic acid represented by SEQ ID Nos: 1-544 or a sequence complementary thereto, the marker nucleic acid being one which is expressed at a given control level in normal cells of the same tissue type as the test cell, and determining the approximate amount of immunocomplex formation by the antibody and the proteins
10 of the test cell, wherein a statistically significant difference in the amount of the immunocomplex formed with the proteins of a test cell as compared to a normal cell of the same tissue type is an indication that the test cell is cancerous or pre-cancerous.

Another such method includes the steps of: providing an antibody specific for the gene product of a marker nucleic acid sequence represented by SEQ ID Nos 1-
15 544, the gene product being present in cancerous tissue of a given tissue type (e.g., colon tissue) at a level more or less than the level of the gene product in non-cancerous tissue of the same tissue type; obtaining from a patient a first sample of tissue of the given tissue type, which sample potentially includes cancerous cells; providing a second sample of tissue of the same tissue type (which may be from the
20 same patient or from a normal control, e.g. another individual or cultured cells), this second sample containing normal cells and essentially no cancerous cells; contacting the antibody with protein (which may be partially purified, in lysed but unfractionated cells, or in situ) of the first and second samples under conditions permitting immunocomplex formation between the antibody and the marker nucleic acid
25 sequence product present in the samples; and comparing (a) the amount of immunocomplex formation in the first sample, with (b) the amount of immunocomplex formation in the second sample, wherein a statistically significant difference in the amount of immunocomplex formation in the first sample less as compared to the amount of immunocomplex formation in the second sample is
30 indicative of the presence of cancerous cells in the first sample of tissue.

The subject invention further provides a method of determining whether a cell sample obtained from a subject possesses an abnormal amount of marker polypeptide which comprises (a) obtaining a cell sample from the subject, (b) quantitatively

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determining the amount of the marker polypeptide in the sample so obtained, and (c) comparing the amount of the marker polypeptide so determined with a known standard, so as to thereby determine whether the cell sample obtained from the subject possesses an abnormal amount of the marker polypeptide. Such marker polypeptides
5 may be detected by immunohistochemical assays, dot-blot assays, ELISA and the like.

Immunoassays are commonly used to quantitate the levels of proteins in cell samples, and many other immunoassay techniques are known in the art. The invention is not limited to a particular assay procedure, and therefore is intended to
10 include both homogeneous and heterogeneous procedures. Exemplary immunoassays which can be conducted according to the invention include fluorescence polarization immunoassay (FPIA), fluorescence immunoassay (FIA), enzyme immunoassay (EIA), nephelometric inhibition immunoassay (NIA), enzyme linked immunosorbent assay (ELISA), and radioimmunoassay (RIA). An indicator moiety, or label group, can be
15 attached to the subject antibodies and is selected so as to meet the needs of various uses of the method which are often dictated by the availability of assay equipment and compatible immunoassay procedures. General techniques to be used in performing the various immunoassays noted above are known to those of ordinary skill in the art.

In another embodiment, the level of the encoded product, i.e., the product
20 encoded by SEQ ID Nos 1-544 or a sequence complementary thereto, in a biological fluid (e.g., blood or urine) of a patient may be determined as a way of monitoring the level of expression of the marker nucleic acid sequence in cells of that patient. Such a method would include the steps of obtaining a sample of a biological fluid from the patient, contacting the sample (or proteins from the sample) with an antibody specific
25 for a encoded marker polypeptide, and determining the amount of immune complex formation by the antibody, with the amount of immune complex formation being indicative of the level of the marker encoded product in the sample. This determination is particularly instructive when compared to the amount of immune complex formation by the same antibody in a control sample taken from a normal
30 individual or in one or more samples previously or subsequently obtained from the same person.

In another embodiment, the method can be used to determine the amount of marker polypeptide present in a cell, which in turn can be correlated with progression

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of a hyperproliferative disorder, e.g., colon cancer. The level of the marker polypeptide can be used predictively to evaluate whether a sample of cells contains cells which are, or are predisposed towards becoming, transformed cells. Moreover, the subject method can be used to assess the phenotype of cells which are known to be transformed, the phenotyping results being useful in planning a particular therapeutic regimen. For instance, very high levels of the marker polypeptide in sample cells is a powerful diagnostic and prognostic marker for a cancer, such as colon cancer. The observation of marker polypeptide level can be utilized in decisions regarding, e.g., the use of more aggressive therapies.

10 As set out above, one aspect of the present invention relates to diagnostic assays for determining, in the context of cells isolated from a patient, if the level of a marker polypeptide is significantly reduced in the sample cells. The term "significantly reduced" refers to a cell phenotype wherein the cell possesses a reduced cellular amount of the marker polypeptide relative to a normal cell of similar tissue origin. For example, a cell may have less than about 50%, 25%, 10%, or 5% of the marker polypeptide that a normal control cell. In particular, the assay evaluates the level of marker polypeptide in the test cells, and, preferably, compares the measured level with marker polypeptide detected in at least one control cell, e.g., a normal cell and/or a transformed cell of known phenotype.

20 Of particular importance to the subject invention is the ability to quantitate the level of marker polypeptide as determined by the number of cells associated with a normal or abnormal marker polypeptide level. The number of cells with a particular marker polypeptide phenotype may then be correlated with patient prognosis. In one embodiment of the invention, the marker polypeptide phenotype of the lesion is determined as a percentage of cells in a biopsy which are found to have abnormally high/low levels of the marker polypeptide. Such expression may be detected by immunohistochemical assays, dot-blot assays, ELISA and the like.

25 Where tissue samples are employed, immunohistochemical staining may be used to determine the number of cells having the marker polypeptide phenotype. For such staining, a multiblock of tissue is taken from the biopsy or other tissue sample and subjected to proteolytic hydrolysis, employing such agents as protease K or pepsin. In certain embodiments, it may be desirable to isolate a nuclear fraction from the sample cells and detect the level of the marker polypeptide in the nuclear fraction.

The tissue samples are fixed by treatment with a reagent such as formalin, glutaraldehyde, methanol, or the like. The samples are then incubated with an antibody, preferably a monoclonal antibody, with binding specificity for the marker polypeptides. This antibody may be conjugated to a label for subsequent detection of binding. Samples are incubated for a time sufficient for formation of the immuno-complexes. Binding of the antibody is then detected by virtue of a label conjugated to this antibody. Where the antibody is unlabeled, a second labeled antibody may be employed, e.g., which is specific for the isotype of the anti-marker polypeptide antibody. Examples of labels which may be employed include radionuclides, fluorescers, chemilumescers, enzymes and the like.

Where enzymes are employed, the substrate for the enzyme may be added to the samples to provide a colored or fluorescent product. Examples of suitable enzymes for use in conjugates include horseradish peroxidase, alkaline phosphatase, malate dehydrogenase and the like. Where not commercially available, such antibody-enzyme conjugates are readily produced by techniques known to those skilled in the art.

In one embodiment, the assay is performed as a dot blot assay. The dot blot assay finds particular application where tissue samples are employed as it allows determination of the average amount of the marker polypeptide associated with a single cell by correlating the amount of marker polypeptide in a cell-free extract produced from a predetermined number of cells.

It is well established in the cancer literature that tumor cells of the same type (e.g., breast and/or colon tumor cells) may not show uniformly increased expression of individual oncogenes or uniformly decreased expression of individual tumor suppressor genes. There may also be varying levels of expression of a given marker gene even between cells of a given type of cancer, further emphasizing the need for reliance on a battery of tests rather than a single test. Accordingly, in one aspect, the invention provides for a battery of tests utilizing a number of probes of the invention, in order to improve the reliability and/or accuracy of the diagnostic test.

In one embodiment, the present invention also provides a method wherein nucleic acid probes are immobilized on a DNA chip in an organized array. Oligonucleotides can be bound to a solid support by a variety of processes, including lithography. For example a chip can hold up to 250,000 oligonucleotides (GeneChip,

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Affymetrix). These nucleic acid probes comprise a nucleotide sequence at least about 12 nucleotides in length, preferably at least about 15 nucleotides, more preferably at least about 25 nucleotides, and most preferably at least about 40 nucleotides, and up to all or nearly all of a sequence which is complementary to a portion of the coding sequence of a marker nucleic acid sequence represented by SEQ ID Nos: 1-544 and is differentially expressed in tumor cells, such as colon cancer cells. The present invention provides significant advantages over the available tests for various cancers, such as colon cancer, because it increases the reliability of the test by providing an array of nucleic acid markers on a single chip.

10 The method includes obtaining a biopsy, which is optionally fractionated by cryostat sectioning to enrich tumor cells to about 80% of the total cell population. The DNA or RNA is then extracted, amplified, and analyzed with a DNA chip to determine the presence or absence of the marker nucleic acid sequences.

In one embodiment, the nucleic acid probes are spotted onto a substrate in a two-dimensional matrix or array. Samples of nucleic acids can be labeled and then hybridized to the probes. Double-stranded nucleic acids, comprising the labeled sample nucleic acids bound to probe nucleic acids, can be detected once the unbound portion of the sample is washed away.

The probe nucleic acids can be spotted on substrates including glass, nitrocellulose, etc. The probes can be bound to the substrate by either covalent bonds or by non-specific interactions, such as hydrophobic interactions. The sample nucleic acids can be labeled using radioactive labels, fluorophores, chromophores, etc.

Techniques for constructing arrays and methods of using these arrays are described in EP No. 0 799 897; PCT No. WO 97/29212; PCT No. WO 97/27317; EP No. 0 785 280; PCT No. WO 97/02357; U.S. Pat. No. 5,593,839; U.S. Pat. No. 5,578,832; EP No. 0 728 520; U.S. Pat. No. 5,599,695; EP No. 0 721 016; U.S. Pat. No. 5,556,752; PCT No. WO 95/22058; and U.S. Pat. No. 5,631,734.

Further, arrays can be used to examine differential expression of genes and can be used to determine gene function. For example, arrays of the instant nucleic acid sequences can be used to determine if any of the nucleic acid sequences are differentially expressed between normal cells and cancer cells, for example. High expression of a particular message in a cancer cell, which is not observed in a corresponding normal cell, can indicate a cancer specific protein.

In yet another embodiment, the invention contemplates using a panel of antibodies which are generated against the marker polypeptides of this invention, which polypeptides are encoded by SEQ ID Nos: 1-544. Such a panel of antibodies may be used as a reliable diagnostic probe for colon cancer. The assay of the present invention comprises contacting a biopsy sample containing cells, e.g., colon cells, with a panel of antibodies to one or more of the encoded products to determine the presence or absence of the marker polypeptides.

The diagnostic methods of the subject invention may also be employed as follow-up to treatment, e.g., quantitation of the level of marker polypeptides may be indicative of the effectiveness of current or previously employed cancer therapies as well as the effect of these therapies upon patient prognosis.

Accordingly, the present invention makes available diagnostic assays and reagents for detecting gain and/or loss of marker polypeptides from a cell in order to aid in the diagnosis and phenotyping of proliferative disorders arising from, for example, tumorigenic transformation of cells.

The diagnostic assays described above can be adapted to be used as prognostic assays, as well. Such an application takes advantage of the sensitivity of the assays of the invention to events which take place at characteristic stages in the progression of a tumor. For example, a given marker gene may be up- or downregulated at a very early stage, perhaps before the cell is irreversibly committed to developing into a malignancy, while another marker gene may be characteristically up or down regulated only at a much later stage. Such a method could involve the steps of contacting the mRNA of a test cell with a nucleic acid probe derived from a given marker nucleic acid which is expressed at different characteristic levels in cancerous or precancerous cells at different stages of tumor progression, and determining the approximate amount of hybridization of the probe to the mRNA of the cell, such amount being an indication of the level of expression of the gene in the cell, and thus an indication of the stage of tumor progression of the cell; alternatively, the assay can be carried out with an antibody specific for the gene product of the given marker nucleic acid, contacted with the proteins of the test cell. A battery of such tests will disclose not only the existence and location of a tumor, but also will allow the clinician to select the mode of treatment most appropriate for the tumor, and to predict the likelihood of success of that treatment.

The methods of the invention can also be used to follow the clinical course of a tumor. For example, the assay of the invention can be applied to a tissue sample from a patient; following treatment of the patient for the cancer, another tissue sample is taken and the test repeated. Successful treatment will result in either removal of all
5 cells which demonstrate differential expression characteristic of the cancerous or precancerous cells, or a substantial increase in expression of the gene in those cells, perhaps approaching or even surpassing normal levels.

In yet another embodiment, the invention provides methods for determining whether a subject is at risk for developing a disease, such as a predisposition to
10 develop cancer, for example colon cancer, associated with an aberrant activity of any one of the polypeptides encoded by nucleic acids of SEQ ID Nos: 1-544, wherein the aberrant activity of the polypeptide is characterized by detecting the presence or absence of a genetic lesion characterized by at least one of (i) an alteration affecting the integrity of a gene encoding a marker polypeptides, or (ii) the mis-expression of
15 the encoding nucleic acid. To illustrate, such genetic lesions can be detected by ascertaining the existence of at least one of (i) a deletion of one or more nucleotides from the nucleic acid sequence, (ii) an addition of one or more nucleotides to the nucleic acid sequence, (iii) a substitution of one or more nucleotides of the nucleic acid sequence, (iv) a gross chromosomal rearrangement of the nucleic acid sequence,
20 (v) a gross alteration in the level of a messenger RNA transcript of the nucleic acid sequence, (vii) aberrant modification of the nucleic acid sequence, such as of the methylation pattern of the genomic DNA, (vii) the presence of a non-wild type splicing pattern of a messenger RNA transcript of the gene, (viii) a non-wild type level of the marker polypeptide, (ix) allelic loss of the gene, and/or (x) inappropriate
25 post-translational modification of the marker polypeptide.

The present invention provides assay techniques for detecting lesions in the encoding nucleic acid sequence. These methods include, but are not limited to, methods involving sequence analysis, Southern blot hybridization, restriction enzyme site mapping, and methods involving detection of absence of nucleotide pairing
30 between the nucleic acid to be analyzed and a probe.

Specific diseases or disorders, e.g., genetic diseases or disorders, are associated with specific allelic variants of polymorphic regions of certain genes, which do not necessarily encode a mutated protein. Thus, the presence of a specific

allelic variant of a polymorphic region of a gene in a subject can render the subject susceptible to developing a specific disease or disorder. Polymorphic regions in genes, can be identified, by determining the nucleotide sequence of genes in populations of individuals. If a polymorphic region is identified, then the link with a specific disease can be determined by studying specific populations of individuals, e.g., individuals which developed a specific disease, such as colon cancer. A polymorphic region can be located in any region of a gene, e.g., exons, in coding or non coding regions of exons, introns, and promoter region.

In an exemplary embodiment, there is provided a nucleic acid composition comprising a nucleic acid probe including a region of nucleotide sequence which is capable of hybridizing to a sense or antisense sequence of a gene or naturally occurring mutants thereof, or 5' or 3' flanking sequences or intronic sequences naturally associated with the subject genes or naturally occurring mutants thereof. The nucleic acid of a cell is rendered accessible for hybridization, the probe is contacted with the nucleic acid of the sample, and the hybridization of the probe to the sample nucleic acid is detected. Such techniques can be used to detect lesions or allelic variants at either the genomic or mRNA level, including deletions, substitutions, etc., as well as to determine mRNA transcript levels.

A preferred detection method is allele specific hybridization using probes overlapping the mutation or polymorphic site and having about 5, 10, 20, 25, or 30 nucleotides around the mutation or polymorphic region. In a preferred embodiment of the invention, several probes capable of hybridizing specifically to allelic variants are attached to a solid phase support, e.g., a "chip". Mutation detection analysis using these chips comprising oligonucleotides, also termed "DNA probe arrays" is described e.g., in Cronin et al. (1996) Human Mutation 7:244. In one embodiment, a chip comprises all the allelic variants of at least one polymorphic region of a gene. The solid phase support is then contacted with a test nucleic acid and hybridization to the specific probes is detected. Accordingly, the identity of numerous allelic variants of one or more genes can be identified in a simple hybridization experiment.

In certain embodiments, detection of the lesion comprises utilizing the probe/primer in a polymerase chain reaction (PCR) (see, e.g. U.S. Patent Nos. 4,683,195 and 4,683,202), such as anchor PCR or RACE PCR, or, alternatively, in a ligase chain reaction (LCR) (see, e.g., Landegran *et al.* (1988) *Science* 241:1077-

Alternative amplification methods include: self sustained sequence replication (Guatelli, J.C. *et al.*, 1990, Proc. Natl. Acad. Sci. USA 87:1874-1878), transcriptional
15 amplification system (Kwoh, D.Y. *et al.*, 1989, Proc. Natl. Acad. Sci. USA 86:1173-1177), Q-Beta Replicase (Lizardi, P.M. *et al.*, 1988, Bio/Technology 6:1197), or any other nucleic acid amplification method, followed by the detection of the amplified molecules using techniques well known to those of skill in the art. These detection schemes are especially useful for the detection of nucleic acid molecules if such
20 molecules are present in very low numbers.

In a preferred embodiment of the subject assay, mutations in, or allelic variants, of a gene from a sample cell are identified by alterations in restriction enzyme cleavage patterns. For example, sample and control DNA is isolated, amplified (optionally), digested with one or more restriction endonucleases, and fragment length sizes are determined by gel electrophoresis. Moreover, the use of sequence specific ribozymes (see, for example, U.S. Patent No. 5,498,531) can be used to score for the presence of specific mutations by development or loss of a ribozyme cleavage site.

Another aspect of the invention is directed to the identification of agents
30 capable of modulating the differentiation and proliferation of cells characterized by
aberrant proliferation. In this regard, the invention provides assays for determining
compounds that modulate the expression of the marker nucleic acids (SEQ ID Nos: 1-
544) and/or alter for example, inhibit the bioactivity of the encoded polypeptide.

Several in vivo methods can be used to identify compounds that modulate expression of the marker nucleic acids (SEQ ID Nos: 1-544) and/or alter for example, inhibit the bioactivity of the encoded polypeptide.

Drug screening is performed by adding a test compound to a sample of cells, and monitoring the effect. A parallel sample which does not receive the test compound is also monitored as a control. The treated and untreated cells are then compared by any suitable phenotypic criteria, including but not limited to microscopic analysis, viability testing, ability to replicate, histological examination, the level of a particular RNA or polypeptide associated with the cells, the level of enzymatic activity expressed by the cells or cell lysates, and the ability of the cells to interact with other cells or compounds. Differences between treated and untreated cells indicates effects attributable to the test compound.

Desirable effects of a test compound include an effect on any phenotype that was conferred by the cancer-associated marker nucleic acid sequence. Examples include a test compound that limits the overabundance of mRNA, limits production of the encoded protein, or limits the functional effect of the protein. The effect of the test compound would be apparent when comparing results between treated and untreated cells.

The invention thus also encompasses methods of screening for agents which inhibit expression of the nucleic acid markers (SEQ ID Nos: 1-544) in vitro, comprising exposing a cell or tissue in which the marker nucleic acid mRNA is detectable in cultured cells to an agent in order to determine whether the agent is capable of inhibiting production of the mRNA; and determining the level of mRNA in the exposed cells or tissue, wherein a decrease in the level of the mRNA after exposure of the cell line to the agent is indicative of inhibition of the marker nucleic acid mRNA production.

Alternatively, the screening method may include in vitro screening of a cell or tissue in which marker protein is detectable in cultured cells to an agent suspected of inhibiting production of the marker protein; and determining the level of the marker protein in the cells or tissue, wherein a decrease in the level of marker protein after exposure of the cells or tissue to the agent is indicative of inhibition of marker protein production.

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The invention also encompasses in vivo methods of screening for agents which inhibit expression of the marker nucleic acids, comprising exposing a mammal having tumor cells in which marker mRNA or protein is detectable to an agent suspected of inhibiting production of marker mRNA or protein; and determining the
5 level of marker mRNA or protein in tumor cells of the exposed mammal. A decrease in the level of marker mRNA or protein after exposure of the mammal to the agent is indicative of inhibition of marker nucleic acid expression.

Accordingly, the invention provides a method comprising incubating a cell expressing the marker nucleic acids (SEQ ID Nos: 1-544) with a test compound and
10 measuring the mRNA or protein level. The invention further provides a method for quantitatively determining the level of expression of the marker nucleic acids in a cell population, and a method for determining whether an agent is capable of increasing or decreasing the level of expression of the marker nucleic acids in a cell population. The method for determining whether an agent is capable of increasing or decreasing
15 the level of expression of the marker nucleic acids in a cell population comprises the steps of (a) preparing cell extracts from control and agent-treated cell populations, (b) isolating the marker polypeptides from the cell extracts, (c) quantifying (e.g., in parallel) the amount of an immunocomplex formed between the marker polypeptide and an antibody specific to said polypeptide. The marker polypeptides of this
20 invention may also be quantified by assaying for its bioactivity. Agents that induce increased the marker nucleic acid expression may be identified by their ability to increase the amount of immunocomplex formed in the treated cell as compared with the amount of the immunocomplex formed in the control cell. In a similar manner, agents that decrease expression of the marker nucleic acid may be identified by their
25 ability to decrease the amount of the immunocomplex formed in the treated cell extract as compared to the control cell.

mRNA levels can be determined by Northern blot hybridization. mRNA levels can also be determined by methods involving PCR. Other sensitive methods for measuring mRNA, which can be used in high throughput assays, e.g., a method using
30 a DELFIA endpoint detection and quantification method, are described, e.g., in Webb and Hurskainen (1996) *Journal of Biomolecular Screening* 1:119. Marker protein levels can be determined by immunoprecipitations or immunohistochemistry using an

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antibody that specifically recognizes the protein product encoded by SEQ ID Nos: 1-544.

Agents that are identified as active in the drug screening assay are candidates to be tested for their capacity to block cell proliferation activity. These agents would be useful for treating a disorder involving aberrant growth of cells, especially colon cells.

A variety of assay formats will suffice and, in light of the present disclosure, those not expressly described herein will nevertheless be comprehended by one of ordinary skill in the art. For instance, the assay can be generated in many different formats, and include assays based on cell-free systems, e.g., purified proteins or cell lysates, as well as cell-based assays which utilize intact cells.

In many drug screening programs which test libraries of compounds and natural extracts, high throughput assays are desirable in order to maximize the number of compounds surveyed in a given period of time. Assays of the present invention which are performed in cell-free systems, such as may be derived with purified or semi-purified proteins or with lysates, are often preferred as "primary" screens in that they can be generated to permit rapid development and relatively easy detection of an alteration in a molecular target which is mediated by a test compound. Moreover, the effects of cellular toxicity and/or bioavailability of the test compound can be generally ignored in the *in vitro* system, the assay instead being focused primarily on the effect of the drug on the molecular target as may be manifest in an alteration of binding affinity with other proteins or changes in enzymatic properties of the molecular target.

A. Use of Nucleic Acids as Probes in Mapping and in Tissue Profiling Probes

Polynucleotide probes as described above, e.g., comprising at least 12 contiguous nucleotides selected from the nucleotide sequence of an nucleic acid as shown in SEQ ID Nos. 1-544, preferably SEQ ID Nos. 1-168, even more preferably SEQ ID Nos. 1-35, or a sequence complementary thereto, are used for a variety of purposes, including identification of human chromosomes and determining transcription levels. Additional disclosure about preferred regions of the nucleic acid sequences is found in the accompanying tables.

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The nucleotide probes are labeled, for example, with a radioactive, fluorescent, biotinylated, or chemiluminescent label, and detected by well known methods appropriate for the particular label selected. Protocols for hybridizing nucleotide probes to preparations of metaphase chromosomes are also well known in the art. A nucleotide probe will hybridize specifically to nucleotide sequences in the chromosome preparations which are complementary to the nucleotide sequence of the probe. A probe that hybridizes specifically to a nucleic acid should provide a detection signal at least 5-, 10-, or 20-fold higher than the background hybridization provided with other unrelated sequences.

10 In a non-limiting example, commercial programs are available for identifying regions of chromosomes commonly associated with disease, such as cancer. Nucleic acids of the invention can be used to probe these regions. For example, if, through profile searching, a nucleic acid is identified as corresponding to a gene encoding a kinase, its ability to bind to a cancer-related chromosomal region will suggest its role as a kinase in one or more stages of tumor cell development/growth. Although some experimentation would be required to elucidate the role, the nucleic acid constitutes a new material for isolating a specific protein that has potential for developing a cancer diagnostic or therapeutic.

20 Nucleotide probes are used to detect expression of a gene corresponding to the nucleic acid. For example, in Northern blots, mRNA is separated electrophoretically and contacted with a probe. A probe is detected as hybridizing to an mRNA species of a particular size. The amount of hybridization is quantitated to determine relative amounts of expression, for example under a particular condition. Probes are also used to detect products of amplification by polymerase chain reaction. The products of the reaction are hybridized to the probe and hybrids are detected. Probes are used for in situ hybridization to cells to detect expression. Probes can also be used in vivo for diagnostic detection of hybridizing sequences. Probes are typically labeled with a radioactive isotope. Other types of detectable labels may be used such as chromophores, fluorophores, and enzymes.

30 Expression of specific mRNA can vary in different cell types and can be tissue specific. This variation of mRNA levels in different cell types can be exploited with nucleic acid probe assays to determine tissue types. For example, PCR, branched DNA probe assays, or blotting techniques utilizing nucleic acid probes substantially

identical or complementary to nucleic acids of SEQ ID Nos. 1-544, preferably SEQ ID Nos. 1-168, even more preferably SEQ ID Nos. 1-35, or a sequence complementary thereto, can determine the presence or absence of target cDNA or mRNA.

5 Examples of a nucleotide hybridization assay are described in Urdea *et al.*, PCT WO92/02526 and Urdea *et al.*, U.S. Patent No. 5,124,246, both incorporated herein by reference. The references describe an example of a sandwich nucleotide hybridization assay.

10 Alternatively, the Polymerase Chain Reaction (PCR) is another means for detecting small amounts of target nucleic acids, as described in Mullis *et al.*, *Meth. Enzymol.* (1987) 155:335-350; U.S. Patent No. 4,683,195; and U.S. Patent No. 4,683,202, all incorporated herein by reference. Two primer polynucleotides nucleotides hybridize with the target nucleic acids and are used to prime the reaction. The primers may be composed of sequence within or 3' and 5' to the polynucleotides
15 of the Sequence Listing. Alternatively, if the primers are 3' and 5' to these polynucleotides, they need not hybridize to them or the complements. A thermostable polymerase creates copies of target nucleic acids from the primers using the original target nucleic acids as a template. After a large amount of target nucleic acids is generated by the polymerase, it is detected by methods such as Southern blots. When
20 using the Southern blot method, the labeled probe will hybridize to a polynucleotide of the Sequence Listing or complement.

 Furthermore, mRNA or cDNA can be detected by traditional blotting techniques described in Sambrook *et al.*, "Molecular Cloning: A Laboratory Manual" (New York, Cold Spring Harbor Laboratory, 1989). mRNA or cDNA generated from
25 mRNA using a polymerase enzyme can be purified and separated using gel electrophoresis. The nucleic acids on the gel are then blotted onto a solid support, such as nitrocellulose. The solid support is exposed to a labeled probe and then washed to remove any unhybridized probe. Next, the duplexes containing the labeled probe are detected. Typically, the probe is labeled with radioactivity.

30

Mapping

Nucleic acids of the present invention are used to identify a chromosome on which the corresponding gene resides. Using fluorescence in situ hybridization

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(FISH) on normal metaphase spreads, comparative genomic hybridization allows total genome assessment of changes in relative copy number of DNA sequences. See Schwartz and Samad, *Current Opinions in Biotechnology* (1994) 8:70-74; Kallioniemi *et al.*, *Seminars in Cancer Biology* (1993) 4:41-46; Valdes and Tagle, *Methods in Molecular Biology* (1997) 68:1, Boultonwood, ed., Human Press, Totowa, NJ.

Preparations of human metaphase chromosomes are prepared using standard cytogenetic techniques from human primary tissues or cell lines. Nucleotide probes comprising at least 12 contiguous nucleotides selected from the nucleotide sequence of SEQ ID Nos. 1-544, preferably SEQ ID Nos. 1-168, even more preferably SEQ ID Nos. 1-35, or a sequence complementary thereto, are used to identify the corresponding chromosome. The nucleotide probes are labeled, for example, with a radioactive, fluorescent, biotinylated, or chemiluminescent label, and detected by well known methods appropriate for the particular label selected. Protocols for hybridizing nucleotide probes to preparations of metaphase chromosomes are also well known in the art. A nucleotide probe will hybridize specifically to nucleotide sequences in the chromosome preparations that are complementary to the nucleotide sequence of the probe. A probe that hybridizes specifically to a target gene provides a detection signal at least 5-, 10-, or 20-fold higher than the background hybridization provided with unrelated coding sequences.

Nucleic acids are mapped to particular chromosomes using, for example, radiation hybrids or chromosome-specific hybrid panels. See Leach *et al.*, *Advances in Genetics*, (1995) 33:63-99; Walter *et al.*, *Nature Genetics* (1994) 7:22-28; Walter and Goodfellow, *Trends in Genetics* (1992) 9:352. Panels for radiation hybrid mapping are available from Research Genentics, Inc., Huntsville, Alabama, USA. Databases for markers using various panels are available via the world wide web at <http://F/shgc-www.stanford.edu>; and other locations. The statistical program RHMAP can be used to construct a map based on the data from radiation hybridization with a measure of the relative likelihood of one order versus another. RHMAP is available via the world wide web at <http://www.sph.umich.edu/group/statgen/software>.

Such mapping can be useful in identifying the function of the target gene by its proximity to other genes with known function. Function can also be assigned to the target gene when particular syndromes or diseases map to the same chromosome.

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Tissue Profiling

The nucleic acids of the present invention can be used to determine the tissue type from which a given sample is derived. For example, a metastatic lesion is identified by its developmental organ or tissue source by identifying the expression of a particular marker of that organ or tissue. If a nucleic acid is expressed only in a specific tissue type, and a metastatic lesion is found to express that-nucleic acid, then the developmental source of the lesion has been identified. Expression of a particular nucleic acid is assayed by detection of either the corresponding mRNA or the protein product. Immunological methods, such as antibody staining, are used to detect a particular protein product. Hybridization methods may be used to detect particular mRNA species, including but not limited to in situ hybridization and Northern blotting.

Use of Polymorphisms

A nucleic acid will be useful in forensics, genetic analysis, mapping, and diagnostic applications if the corresponding region of a gene is polymorphic in the human population. A particular polymorphic form of the nucleic acid may be used to either identify a sample as deriving from a suspect or rule out the possibility that the sample derives from the suspect. Any means for detecting a polymorphism in a gene are used, including but not limited to electrophoresis of protein polymorphic variants, differential sensitivity to restriction enzyme cleavage, and hybridization to an allele-specific probe.

B. Use of Nucleic Acids and Encoded Polypeptides to Raise Antibodies

Expression products of a nucleic acid, the corresponding mRNA or cDNA, or the corresponding complete gene are prepared and used for raising antibodies for experimental, diagnostic, and therapeutic purposes. For nucleic acids to which a corresponding gene has not been assigned, this provides an additional method of identifying the corresponding gene. The nucleic acid or related cDNA is expressed as described above, and antibodies are prepared. These antibodies are specific to an epitope on the encoded polypeptide, and can precipitate or bind to the corresponding native protein in a cell or tissue preparation or in a cell-free extract of an in vitro expression system.

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Immunogens for raising antibodies are prepared by mixing the polypeptides encoded by the nucleic acids of the present invention with adjuvants. Alternatively, polypeptides are made as fusion proteins to larger immunogenic proteins.

Polypeptides are also covalently linked to other larger immunogenic proteins, such as
 5 keyhole limpet hemocyanin. Immunogens are typically administered intradermally, subcutaneously, or intramuscularly. Immunogens are administered to experimental animals such as rabbits, sheep, and mice, to generate antibodies. Optionally, the animal spleen cells are isolated and fused with myeloma cells to form hybridomas which secrete monoclonal antibodies. Such methods are well known in the art.
 10 According to another method known in the art, the nucleic acid is administered directly, such as by intramuscular injection, and expressed in vivo. The expressed protein generates a variety of protein-specific immune responses, including production of antibodies, comparable to administration of the protein.

Preparations of polyclonal and monoclonal antibodies specific for nucleic
 15 acid-encoded proteins and polypeptides are made using standard methods known in the art. The antibodies specifically bind to epitopes present in the polypeptides encoded by a nucleic acid of SEQ ID Nos. 1-544, preferably SEQ ID Nos. 1-168, even more preferably SEQ ID Nos. 1-35, or a sequence complementary thereto. In another embodiment, the antibodies specifically bind to epitopes present in a polypeptide
 20 encoded by SEQ ID Nos. 1-544. Typically, at least about 6, 8, 10, or 12 contiguous amino acids are required to form an epitope. However, epitopes which involve non-contiguous amino acids may require more, for example, at least about 15, 25, or 50 amino acids. A short sequence of a nucleic acid may then be unsuitable for use as an epitope to raise antibodies for identifying the corresponding novel protein, because of
 25 the potential for cross-reactivity with a known protein. However, the antibodies may be useful for other purposes, particularly if they identify common structural features of a known protein and a novel polypeptide encoded by a nucleic acid of the invention.

Antibodies that specifically bind to human nucleic acid-encoded polypeptides
 30 should provide a detection signal at least about 5-, 10-, or 20-fold higher than a detection signal provided with other proteins when used in Western blots or other immunochemical assays. Preferably, antibodies that specifically bind nucleic acid T-

encoded polypeptides do not detect other proteins in immunochemical assays and can immunoprecipitate nucleic acid-encoded proteins from solution.

To test for the presence of serum antibodies to the nucleic acid-encoded polypeptide in a human population, human antibodies are purified by methods well
5 known in the art. Preferably, the antibodies are affinity purified by passing antiserum over a column to which a nucleic acid-encoded protein, polypeptide, or fusion protein is bound. The bound antibodies can then be eluted from the column, for example using a buffer with a high salt concentration.

In addition to the antibodies discussed above, genetically engineered antibody
10 derivatives are made, such as single chain antibodies.

Antibodies may be made by using standard protocols known in the art (See, for example, Antibodies: A Laboratory Manual ed. by Harlow and Lane (Cold Spring Harbor Press: 1988)). A mammal, such as a mouse, hamster, or rabbit can be immunized with an immunogenic form of the peptide (e.g., a mammalian polypeptide
15 or an antigenic fragment which is capable of eliciting an antibody response, or a fusion protein as described above).

In one aspect, this invention includes monoclonal antibodies that show a subject polypeptide is highly expressed in colorectal tissue or tumor tissue, especially colon cancer tissue or colon cancer-derived cell lines. Therefore, in one embodiment,
20 this invention provides a diagnostic tool for the analysis of expression of a subject polypeptide in general, and in particular, as a diagnostic for colon cancer.

Techniques for conferring immunogenicity on a protein or peptide include conjugation to carriers or other techniques well known in the art. An immunogenic portion of a protein can be administered in the presence of adjuvant. The progress of
25 immunization can be monitored by detection of antibody titers in plasma or serum. Standard ELISA or other immunoassays can be used with the immunogen as antigen to assess the levels of antibodies. In a preferred embodiment, the subject antibodies are immunospecific for antigenic determinants of a protein of a mammal, e.g., antigenic determinants of a protein encoded by one of SEQ ID Nos. 1-544 or closely
30 related homologs (e.g., at least 90% identical, and more preferably at least 95% identical).

Following immunization of an animal with an antigenic preparation of a polypeptide, antisera can be obtained and, if desired, polyclonal antibodies isolated

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proteins. For instance, gt11 will produce fusion proteins whose amino termini consist of β -galactosidase amino acid sequences and whose carboxyl termini consist of a foreign polypeptide. Antigenic epitopes of a protein, e.g., other orthologs of a particular protein or other paralogs from the same species, can then be detected with
5 antibodies, as, for example, reacting nitrocellulose filters lifted from infected plates with antibodies. Positive phage detected by this assay can then be isolated from the infected plate. Thus, the presence of homologs can be detected and cloned from other animals, as can alternate isoforms (including splicing variants) from humans.

In another embodiment, a panel of monoclonal antibodies may be used,
10 wherein each of the epitope's involved functions are represented by a monoclonal antibody. Loss or perturbation of binding of a monoclonal antibody in the panel would be indicative of a mutational alteration of the protein and thus of the corresponding gene.

15 C. Differential Expression

The present invention also provides a method to identify abnormal or diseased tissue in a human. For nucleic acids corresponding to profiles of protein families as described above, the choice of tissue may be dictated by the putative biological function. The expression of a gene corresponding to a specific nucleic acid is
20 compared between a first tissue that is suspected of being diseased and a second, normal tissue of the human. The normal tissue is any tissue of the human, especially those that express the target gene including, but not limited to, brain, thymus, testis, heart, prostate, placenta, spleen, small intestine, skeletal muscle, pancreas, and the mucosal lining of the colon.

25 The tissue suspected of being abnormal or diseased can be derived from a different tissue type of the human, but preferably it is derived from the same tissue type; for example an intestinal polyp or other abnormal growth should be compared with normal intestinal tissue. A difference between the target gene, mRNA, or protein in the two tissues which are compared, for example in molecular weight, amino acid
30 or nucleotide sequence, or relative abundance, indicates a change in the gene, or a gene which regulates it, in the tissue of the human that was suspected of being diseased.

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The target genes in the two tissues are compared by any means known in the art. For example, the two genes are sequenced, and the sequence of the gene in the tissue suspected of being diseased is compared with the gene sequence in the normal tissue. The target genes, or portions thereof, in the two tissues are amplified, for example using nucleotide primers based on the nucleotide sequence shown in the Sequence Listing, using the polymerase chain reaction. The amplified genes or portions of genes are hybridized to nucleotide probes selected from a corresponding nucleotide sequence shown SEQ ID No. 1-544. A difference in the nucleotide sequence of the target gene in the tissue suspected of being diseased compared with the normal nucleotide sequence suggests a role of the nucleic acid-encoded proteins in the disease, and provides a lead for preparing a therapeutic agent. The nucleotide probes are labeled by a variety of methods, such as radiolabeling, biotinylation, or labeling with fluorescent or chemiluminescent tags, and detected by standard methods known in the art.

Alternatively, target mRNA in the two tissues is compared. PolyA⁺ RNA is isolated from the two tissues as is known in the art. For example, one of skill in the art can readily determine differences in the size or amount of target mRNA transcripts between the two tissues using Northern blots and nucleotide probes selected from the nucleotide sequence shown in the Sequence Listing. Increased or decreased expression of a target mRNA in a tissue sample suspected of being diseased, compared with the expression of the same target mRNA in a normal tissue, suggests that the expressed protein has a role in the disease, and also provides a lead for preparing a therapeutic agent.

Any method for analyzing proteins is used to compare two nucleic acid-encoded proteins from matched samples. The sizes of the proteins in the two tissues are compared, for example, using antibodies of the present invention to detect nucleic acid-encoded proteins in Western blots of protein extracts from the two tissues. Other changes, such as expression levels and subcellular localization, can also be detected immunologically, using antibodies to the corresponding protein. A higher or lower level of nucleic acid-encoded protein expression in a tissue suspected of being diseased, compared with the same nucleic acid-encoded protein expression level in a normal tissue, is indicative that the expressed protein has a role in the disease, and provides another lead for preparing a therapeutic agent.

Similarly, comparison of gene sequences or of gene expression products, e.g., mRNA and protein, between a human tissue that is suspected of being diseased and a normal tissue of a human, are used to follow disease progression or remission in the human. Such comparisons of genes, mRNA, or protein are made as described above.

5 For example, increased or decreased expression of the target gene in the tissue suspected of being neoplastic can indicate the presence of neoplastic cells in the tissue. The degree of increased expression of the target gene in the neoplastic tissue relative to expression of the gene in normal tissue, or differences in the amount of increased expression of the target gene in the neoplastic tissue over time, is used to
10 assess the progression of the neoplasia in that tissue or to monitor the response of the neoplastic tissue to a therapeutic protocol over time.

The expression pattern of any two cell types can be compared, such as low and high metastatic tumor cell lines, or cells from tissue which have and have not been exposed to a therapeutic agent. A genetic predisposition to disease in a human is
15 detected by comparing an target gene, mRNA, or protein in a fetal tissue with a normal target gene, mRNA, or protein. Fetal tissues that are used for this purpose include, but are not limited to, amniotic fluid, chorionic villi, blood, and the blastomere of an in vitro-fertilized embryo. The comparable normal target gene is obtained from any tissue. The mRNA or protein is obtained from a normal tissue of a
20 human in which the target gene is expressed. Differences such as alterations in the nucleotide sequence or size of the fetal target gene or mRNA, or alterations in the molecular weight, amino acid sequence, or relative abundance of fetal target protein, can indicate a germline mutation in the target gene of the fetus, which indicates a genetic predisposition to disease.

25

D. Use of Nucleic Acids and Encoded Polypeptides to Screen for Peptide Analogs and Antagonists

Polypeptides encoded by the instant nucleic acids, e.g., SEQ ID Nos. 1-544,
30 preferably SEQ ID Nos. 1-168, even more preferably SEQ ID Nos. 1-35, or a sequence complementary thereto, and corresponding full length genes can be used to screen peptide libraries to identify binding partners, such as receptors, from among the encoded polypeptides.

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A library of peptides may be synthesized following the methods disclosed in U.S. Pat. No. 5,010,175, and in PCT WO 91/17823. As described below in brief, one prepares a mixture of peptides, which is then screened to identify the peptides exhibiting the desired signal transduction and receptor binding activity. In the '175 method, a suitable peptide synthesis support (e.g., a resin) is coupled to a mixture of appropriately protected, activated amino acids. The concentration of each amino acid in the reaction mixture is balanced or adjusted in inverse proportion to its coupling reaction rate so that the product is an equimolar mixture of amino acids coupled to the starting resin. The bound amino acids are then deprotected, and reacted with another balanced amino acid mixture to form an equimolar mixture of all possible dipeptides. This process is repeated until a mixture of peptides of the desired length (e.g., hexamers) is formed. Note that one need not include all amino acids in each step: one may include only one or two amino acids in some steps (e.g., where it is known that a particular amino acid is essential in a given position), thus reducing the complexity of the mixture. After the synthesis of the peptide library is completed, the mixture of peptides is screened for binding to the selected polypeptide. The peptides are then tested for their ability to inhibit or enhance activity. Peptides exhibiting the desired activity are then isolated and sequenced.

The method described in WO 91/17823 is similar. However, instead of reacting the synthesis resin with a mixture of activated amino acids, the resin is divided into twenty equal portions (or into a number of portions corresponding to the number of different amino acids to be added in that step), and each amino acid is coupled individually to its portion of resin. The resin portions are then combined, mixed, and again divided into a number of equal portions for reaction with the second amino acid. In this manner, each reaction may be easily driven to completion. Additionally, one may maintain separate "subpools" by treating portions in parallel, rather than combining all resins at each step. This simplifies the process of determining which peptides are responsible for any observed receptor binding or signal transduction activity.

In such cases, the subpools containing, e.g., 1-2,000 candidates each are exposed to one or more polypeptides of the invention. Each subpool that produces a positive result is then resynthesized as a group of smaller subpools (sub-subpools) containing, e.g., 20-100 candidates, and reassayed. Positive sub-subpools may be

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resynthesized as individual compounds, and assayed finally to determine the peptides that exhibit a high binding constant. These peptides can be tested for their ability to inhibit or enhance the native activity. The methods described in WO 91/7823 and U.S. Patent No. 5,194,392 (herein incorporated by reference) enable the preparation of
5 such pools and subpools by automated techniques in parallel, such that all synthesis and resynthesis may be performed in a matter of days.

Peptide agonists or antagonists are screened using any available method, such as signal transduction, antibody binding, receptor binding, mitogenic assays, chemotaxis assays, etc. The methods described herein are presently preferred. The
10 assay conditions ideally should resemble the conditions under which the native activity is exhibited *in vivo*, that is, under physiologic pH, temperature, and ionic strength. Suitable agonists or antagonists will exhibit strong inhibition or enhancement of the native activity at concentrations that do not cause toxic side effects in the subject. Agonists or antagonists that compete for binding to the native
15 polypeptide may require concentrations equal to or greater than the native concentration, while inhibitors capable of binding irreversibly to the polypeptide may be added in concentrations on the order of the native concentration.

The end results of such screening and experimentation will be at least one novel polypeptide binding partner, such as a receptor, encoded by a nucleic acid of the
20 invention, and at least one peptide agonist or antagonist of the novel binding partner. Such agonists and antagonists can be used to modulate, enhance, or inhibit receptor function in cells to which the receptor is native, or in cells that possess the receptor as a result of genetic engineering. Further, if the novel receptor shares biologically important characteristics with a known receptor, information about agonist/antagonist
25 binding may help in developing improved agonists/antagonists of the known receptor.

E. Pharmaceutical Compositions and Therapeutic Uses

Pharmaceutical compositions can comprise polypeptides, antibodies, or polynucleotides of the claimed invention. The pharmaceutical compositions will
30 comprise a therapeutically effective amount of either polypeptides, antibodies, or polynucleotides of the claimed invention.

The term "therapeutically effective amount" as used herein refers to an amount of a therapeutic agent to treat, ameliorate, or prevent a desired disease or condition, or

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to exhibit a detectable therapeutic or preventative effect. The effect can be detected by, for example, chemical markers or antigen levels. Therapeutic effects also include reduction in physical symptoms, such as decreased body temperature. The precise effective amount for a subject will depend upon the subject's size and health, the nature and extent of the condition, and the therapeutics or combination of therapeutics selected for administration. Thus, it is not useful to specify an exact effective amount in advance. However, the effective amount for a given situation can be determined by routine experimentation and is within the judgment of the clinician.

For purposes of the present invention, an effective dose will be from about 0.01 mg/ kg to 50 mg/kg or 0.05 mg/kg to about 10 mg/kg of the DNA constructs in the individual to which it is administered.

A pharmaceutical composition can also contain a pharmaceutically acceptable carrier. The term "pharmaceutically acceptable carrier" refers to a carrier for administration of a therapeutic agent, such as antibodies or a polypeptide, genes, and other therapeutic agents. The term refers to any pharmaceutical carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition, and which may be administered without undue toxicity. Suitable carriers may be large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, and inactive virus particles. Such carriers are well known to those of ordinary skill in the art.

Pharmaceutically acceptable salts can be used therein, for example, mineral acid salts such as hydrochlorides, hydrobromides, phosphates, sulfates, and the like; and the salts of organic acids such as acetates, propionates, malonates, benzoates, and the like. A thorough discussion of pharmaceutically acceptable excipients is available in *Remington's Pharmaceutical Sciences* (Mack Pub. Co., N.J. 1991).

Pharmaceutically acceptable carriers in therapeutic compositions may contain liquids such as water, saline, glycerol and ethanol. Additionally, auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, may be present in such vehicles. Typically, the therapeutic compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection may also be prepared. Liposomes are included within the definition of a pharmaceutically acceptable carrier.

Delivery Methods

Once formulated, the nucleic acid compositions of the invention can be (1) administered directly to the subject; (2) delivered ex vivo, to cells derived from the
5 subject; or (3) delivered in vitro for expression of recombinant proteins.

Direct delivery of the compositions will generally be accomplished by injection, either subcutaneously, intraperitoneally, intravenously or intramuscularly, or delivered to the interstitial space of a tissue. The compositions can also be administered into a tumor or lesion. Other modes of administration include oral and
10 pulmonary administration, suppositories, and transdermal applications, needles, and gene guns or hyposprays. Dosage treatment may be a single dose schedule or a multiple dose schedule.

Methods for the ex vivo delivery and reimplantation of transformed cells into a subject are known in the art and described in e.g., International Publication No. WO
15 93/14778. Examples of cells useful in ex vivo applications include, for example, stem cells, particularly hematopoietic, lymph cells, macrophages, dendritic cells, or tumor cells.

Generally, delivery of nucleic acids for both ex vivo and in vitro applications can be accomplished by, for example, dextran-mediated transfection, calcium
20 phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei, all well known in the art.

Once a subject gene has been found to correlate with a proliferative disorder, such as neoplasia, dysplasia, and hyperplasia, the disorder may be amenable to
25 treatment by administration of a therapeutic agent based on the nucleic acid or corresponding polypeptide.

Preparation of antisense polypeptides is discussed above. Neoplasias that are treated with the antisense composition include, but are not limited to, cervical cancers, melanomas, colorectal adenocarcinomas, Wilms' tumor, retinoblastoma, sarcomas,
30 myosarcomas, lung carcinomas, leukemias, such as chronic myelogenous leukemia, promyelocytic leukemia, monocytic leukemia, and myeloid leukemia, and lymphomas, such as histiocytic lymphoma. Proliferative disorders that are treated with the therapeutic composition include disorders such as anhydric hereditary

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ectodermal dysplasia, congenital alveolar dysplasia, epithelial dysplasia of the cervix, fibrous dysplasia of bone, and mammary dysplasia. Hyperplasias, for example, endometrial, adrenal, breast, prostate, or thyroid hyperplasias or pseudoepitheliomatous hyperplasia of the skin, are treated with antisense therapeutic compositions. Even in disorders in which mutations in the corresponding gene are not implicated, downregulation or inhibition of nucleic acid-related gene expression can have therapeutic application. For example, decreasing nucleic acid-related gene expression can help to suppress tumors in which enhanced expression of the gene is implicated.

Both the dose of the antisense composition and the means of administration are determined based on the specific qualities of the therapeutic composition, the condition, age, and weight of the patient, the progression of the disease, and other relevant factors. Administration of the therapeutic antisense agents of the invention includes local or systemic administration, including injection, oral administration, particle gun or catheterized administration, and topical administration. Preferably, the therapeutic antisense composition contains an expression construct comprising a promoter and a polynucleotide segment of at least about 12, 22, 25, 30, or 35 contiguous nucleotides of the antisense strand of a nucleic acid. Within the expression construct, the polynucleotide segment is located downstream from the promoter, and transcription of the polynucleotide segment initiates at the promoter.

Various methods are used to administer the therapeutic composition directly to a specific site in the body. For example, a small metastatic lesion is located and the therapeutic composition injected several times in several different locations within the body of tumor. Alternatively, arteries which serve a tumor are identified, and the therapeutic composition injected into such an artery, in order to deliver the composition directly into the tumor. A tumor that has a necrotic center is aspirated and the composition injected directly into the now empty center of the tumor. The antisense composition is directly administered to the surface of the tumor, for example, by topical application of the composition. X-ray imaging is used to assist in certain of the above delivery methods.

Receptor-mediated targeted delivery of therapeutic compositions containing an antisense polynucleotide, subgenomic polynucleotides, or antibodies to specific tissues is also used. Receptor-mediated DNA delivery techniques are described in, for

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example, Findeis *et al.*, *Trends in Biotechnol.* (1993) 11:202-205; Chiou *et al.*, (1994) Gene Therapeutics: Methods And Applications Of Direct Gene Transfer (J.A. Wolff, ed.); Wu & Wu, *J. Biol. Chem.* (1988) 263:621-24; Wu *et al.*, *J. Biol. Chem.* (1994) 269:542-46; Zenke *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1990) 87:3655-59; Wu *et al.*,
5 *J. Biol. Chem.* (1991) 266:338-42. Preferably, receptor-mediated targeted delivery of therapeutic compositions containing antibodies of the invention is used to deliver the antibodies to specific tissue.

Therapeutic compositions containing antisense subgenomic polynucleotides are administered in a range of about 100 ng to about 200 mg of DNA for local
10 administration in a gene therapy protocol. Concentration ranges of about 500 ng to about 50 mg, about 1 mg to about 2 mg, about 5 mg to about 500 mg, and about 20 mg to about 100 mg of DNA can also be used during a gene therapy protocol. Factors such as method of action and efficacy of transformation and expression are considerations which will affect the dosage required for ultimate efficacy of the
15 antisense subgenomic nucleic acids. Where greater expression is desired over a larger area of tissue, larger amounts of antisense subgenomic nucleic acids or the same amounts readministered in a successive protocol of administrations, or several administrations to different adjacent or close tissue portions of, for example, a tumor site, may be required to effect a positive therapeutic outcome. In all cases, routine
20 experimentation in clinical trials will determine specific ranges for optimal therapeutic effect. A more complete description of gene therapy vectors, especially retroviral vectors, is contained in U.S. Serial No. 08/869,309, which is expressly incorporated herein, and in section F below.

For genes encoding polypeptides or proteins with anti-inflammatory activity,
25 suitable use, doses, and administration are described in U.S. Patent No. 5,654,173, incorporated herein by reference. Therapeutic agents also include antibodies to proteins and polypeptides encoded by the subject nucleic acids, as described in U.S. Patent No. 5,654,173.

30 F. Gene Therapy

The therapeutic nucleic acids of the present invention may be utilized in gene delivery vehicles. The gene delivery vehicle may be of viral or non-viral origin (see generally, Jolly, *Cancer Gene Therapy* (1994) 1:51-64; Kimura, *Human Gene*

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Therpay (1994) 5:845-852; Connelly, *Human Gene Therapy* (1995) 1:185-193; and Kaplitt, *Nature Genetics* (1994) 6:148-153). Gene therapy vehicles for delivery of constructs including a coding sequence of a therapeutic of the invention can be administered either locally or systemically. These constructs can utilize viral or non-viral vector approaches. Expression of such coding sequences can be induced using endogenous mammalian or heterologous promoters. Expression of the coding sequence can be either constitutive or regulated.

The present invention can employ recombinant retroviruses which are constructed to carry or express a selected nucleic acid molecule of interest. Retrovirus vectors that can be employed include those described in EP 0 415 731; WO 90/07936; WO 94/03622; WO 93/25698; WO 93/25234; U.S. Patent No. 5, 219,740; WO 93/11230; WO 93/10218; Vile and Hart, *Cancer Res.* (1993) 53:3860-3864; Vile and Hart, *Cancer Res.* (1993) 53:962-967; Ram et al., *Cancer Res.* (1993) 53:83-88; Takamiya et al., *J. Neurosci. Res.* (1992) 33:493-503; Baba et al., *J. Neurosurg.* (1993) 79:729-735; U.S. Patent no. 4,777,127; GB Patent No. 2,200,651; and EP 0 345 242. Preferred recombinant retroviruses include those described in WO 91/02805.

Packaging cell lines suitable for use with the above-described retroviral vector constructs may be readily prepared (see PCT publications WO 95/30763 and WO 92/05266), and used to create producer cell lines (also termed vector cell lines) for the production of recombinant vector particles. Within particularly preferred embodiments of the invention, packaging cell lines are made from human (such as HT1080 cells) or mink parent cell lines, thereby allowing production of recombinant retroviruses that can survive inactivation in human serum.

The present invention also employs alphavirus-based vectors that can function as gene delivery vehicles. Such vectors can be constructed from a wide variety of alphaviruses, including, for example, Sindbis virus vectors, Semliki forest virus (ATCC VR-67; ATCC VR-1247), Ross River virus (ATCC VR-373; ATCC VR-1246) and Venezuelan equine encephalitis virus (ATCC VR-923; ATCC VR-1250; ATCC VR 1249; ATCC VR-532). Representative examples of such vector systems include those described in U.S. Patent Nos. 5,091,309; 5,217,879; and 5,185,440; and PCT Publication Nos. WO 92/10578; WO 94/21792; WO 95/27069; WO 95/27044; and WO 95/07994.

Gene delivery vehicles of the present invention can also employ parvovirus such as adeno-associated virus (AAV) vectors. Representative examples include the AAV vectors disclosed by Srivastava in WO 93/09239, Samulski et al., *J. Vir.* (1989) 63:3822-3828; Mendelson et al., *Viol.* (1988) 166:154-165; and Flotte et al., *PNAS* (1993) 90:10613-10617.

Representative examples of adenoviral vectors include those described by Berkner, *Biotechniques* (1988) 6:616-627; Rosenfeld et al., *Science* (1991) 252:431-434; WO 93/19191; Kolls et al., *PNAS* (1994) 91:215-219; Kass-Eisler et al., *PNAS* (1993) 90:11498-11502; Guzman et al., *Circulation* (1993) 88:2838-2848; Guzman et al., *Cir. Res.* (1993) 73:1202-1207; Zabner et al., *Cell* (1993) 75:207-216; Li et al., *Hum. Gene Ther.* (1993) 4:403-409; Cailaud et al., *Eur. J. Neurosci.* (1993) 5:1287-1291; Vincent et al., *Nat. Genet.* (1993) 5:130-134; Jaffe et al., *Nat. Genet.* (1992) 1:372-378; and Levrero et al., *Gene* (1991) 101:195-202. Exemplary adenoviral gene therapy vectors employable in this invention also include those described in WO 94/12649, WO 93/03769; WO 93/19191; WO 94/28938; WO 95/11984 and WO 95/00655. Administration of DNA linked to killed adenovirus as described in Curiel, *Hum. Gene Ther.* (1992) 3:147-154 may be employed.

Other gene delivery vehicles and methods may be employed, including polycationic condensed DNA linked or unlinked to killed adenovirus alone, for example Curiel, *Hum. Gene Ther.* (1992) 3:147-154; ligand linked DNA, for example see Wu, *J. Biol. Chem.* (1989) 264:16985-16987; eukaryotic cell delivery vehicles cells, for example see U.S. Serial No. 08/240,030, filed May 9, 1994, and U.S. Serial No. 08/404,796; deposition of photopolymerized hydrogel materials; hand-held gene transfer particle gun, as described in U.S. Patent No. 5,149,655; ionizing radiation as described in U.S. Patent No. 5,206,152 and in WO92/11033; nucleic charge neutralization or fusion with cell membranes. Additional approaches are described in Philip, *Mol. Cell Biol.* (1994) 14:2411-2418, and in Woffendin, *Proc. Natl. Acad. Sci.* (1994) 91:1581-1585.

Naked DNA may also be employed. Exemplary naked DNA introduction methods are described in WO 90/11092 and U.S. Patent No. 5,580,859. Uptake efficiency may be improved using biodegradable latex beads. DNA coated latex beads are efficiently transported into cells after endocytosis initiation by the beads. The method may be improved further by treatment of the beads to increase

Further non-viral delivery suitable for use includes mechanical delivery systems such as the approach described in Woffendin *et al.*, *Proc. Natl. Acad. Sci. USA* (1994) 91(24):11581-11585. Moreover, the coding sequence and the product of expression of such can be delivered through deposition of photopolymerized hydrogel materials. Other conventional methods for gene delivery that can be used for delivery of the coding sequence include, for example, use of hand-held gene transfer particle gun, as described in U.S. Patent No. 5,149,655; use of ionizing radiation for activating transferred gene, as described in U.S. Patent No. 5,206,152 and PCT No. WO 92/11033.

One aspect of the present invention relates to transgenic non-human animals having germline and/or somatic cells in which the biological activity of one or more genes are altered by a chromosomally incorporated transgene.

Yet another preferred transgenic animal includes a transgene encoding an antisense transcript which, when transcribed from the transgene, hybridizes with a gene or a mRNA transcript thereof, and inhibits expression of the gene.

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growth factor. A genetically altered mouse of this type is able to serve as a useful model for hereditary cancers and as a test animal for carcinogen studies. The invention additionally pertains to the use of such non-human animals or animal cells, and their progeny in research and medicine.

5 Furthermore, it is contemplated that cells of the transgenic animals of the present invention can include other transgenes, e.g., which alter the biological activity of a second tumor suppressor gene or an oncogene. For instance, the second transgene can functionally disrupt the biological activity of a second tumor suppressor gene, such as p53, p73, DCC, p21^{cip1}, p27^{kip1}, Rb, Mad or E2F. Alternatively, the
10 second transgene can cause overexpression or loss of regulation of an oncogene, such as ras, myc, a cdc25 phosphatase, Bcl-2, Bcl-6, a transforming growth factor, neu, int-3, polyoma virus middle T antigen, SV40 large T antigen, a papillomaviral E6 protein, a papillomaviral E7 protein, CDK4, or cyclin D1.

 A preferred transgenic non-human animal of the present invention has
15 germline and/or somatic cells in which one or more alleles of a gene are disrupted by a chromosomally incorporated transgene, wherein the transgene includes a marker sequence providing a detectable signal for identifying the presence of the transgene in cells of the transgenic animal, and replaces at least a portion of the gene or is inserted into the gene or disrupts expression of a wild-type protein.

20 Still another aspect of the present invention relates to methods for generating non-human animals and stem cells having a functionally disrupted endogenous gene. In a preferred embodiment, the method comprises the steps of:

- (i) constructing a transgene construct including (a) a recombination region having at least a portion of the gene, which recombination region directs
25 recombination of the transgene with the gene, and (b) a marker sequence which provides a detectable signal for identifying the presence of the transgene in a cell;
- (ii) transferring the transgene into stem cells of a non-human animal;
- (iii) selecting stem cells having a correctly targeted homologous recombination
30 between the transgene and the gene;
- (iv) transferring cells identified in step (iii) into a non-human blastocyst and implanting the resulting chimeric blastocyst into a non-human female; and

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- (v) collecting offspring harboring an endogenous gene allele having the correctly targeted recombination.

Yet another aspect of the invention provides a method for evaluating the carcinogenic potential of an agent by (i) contacting a transgenic animal of the present invention with a test agent, and (ii) comparing the number of transformed cells in a sample from the treated animal with the number of transformed cells in a sample from an untreated transgenic animal or transgenic animal treated with a control agent. The difference in the number of transformed cells in the treated animal, relative to the number of transformed cells in the absence of treatment with a control agent, indicates the carcinogenic potential of the test compound.

Another aspect of the invention provides a method of evaluating an anti-proliferative activity of a test compound. In preferred embodiments, the method includes contacting a transgenic animal of the present invention, or a sample of cells from such animal, with a test agent, and determining the number of transformed cells in a specimen from the transgenic animal or in the sample of cells. A statistically significant decrease in the number of transformed cells, relative to the number of transformed cells in the absence of the test agent, indicates the test compound is a potential anti-proliferative agent.

The practice of the present invention will employ, unless otherwise indicated, conventional techniques of cell biology, cell culture, molecular biology, transgenic biology, microbiology, recombinant DNA, and immunology, which are within the skill of the art. Such techniques are explained fully in the literature. See, for example, *Molecular Cloning A Laboratory Manual*, 2nd Ed., ed. by Sambrook, Fritsch and Maniatis (Cold Spring Harbor Laboratory Press:1989); *DNA Cloning*, Volumes I and II (D. N. Glover ed., 1985); *Oligonucleotide Synthesis* (M. J. Gait ed., 1984); Mullis *et al.* U.S. Patent No. 4,683,195; *Nucleic Acid Hybridization* (B.D. Hames & S. J. Higgins eds. 1984); *Transcription And Translation* (B. D. Hames & S. J. Higgins eds. 1984); *Culture Of Animal Cells* (R. I. Freshney, Alan R. Liss, Inc., 1987); *Immobilized Cells And Enzymes* (IRL Press, 1986); B. Perbal, *A Practical Guide To Molecular Cloning* (1984); the treatise, *Methods In Enzymology* (Academic Press, Inc., N.Y.); *Gene Transfer Vectors For Mammalian Cells* (J. H. Miller and M. P. Calos eds., 1987, Cold Spring Harbor Laboratory); *Methods In Enzymology*, Vols. 154 and 155 (Wu et al. eds.), *Immunochemical Methods In Cell And Molecular*

Biology (Mayer and Walker, eds., Academic Press, London, 1987); *Handbook Of Experimental Immunology*, Volumes I-IV (D. M. Weir and C. C. Blackwell, eds., 1986); *Manipulating the Mouse Embryo*, (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1986).

5 As mentioned above, the sequences described herein are believed to have particular utility in regards to colon cancer. However, they may also be useful with other types of cancers and other disease states.

The present invention will now be illustrated by reference to the following examples which set forth particularly advantageous embodiments. However, it should
10 be noted that these embodiments are illustrative and are not to be construed as restricting the invention in any way.

XI. Examples

A. Identification of differentially expressed sequences.

15

Description of the Libraries

SEQ ID Nos: 1-544 were derived from libraries designated as DE and PA as described below. The DE library is a normalized, colon cancer specific, subtracted cDNA library. The DE library is specific for sequences expressed in colon cancer
20 [proximal and distal Dukes' B, microsatellite instability negative (MSI-)] but not expressed in normal tissues, including normal colon tissue. The PA library is a normalized, colon specific, subtracted cDNA library. The PA library is specific for sequences expressed in normal colon tissue but not expressed in other normal tissues.

25 Construction of a colon cancer specific library

A subtracted colon cancer specific library was made by subtracting pooled proximal, stage B, MSI⁻ and distal, Stage B, MSI⁻ tumor tissue cDNA against a combination of pooled driver normal cDNA made from colon, peripheral blood leukocytes (PBL), liver, spleen, lung, kidney, heart, small intestine, skeletal muscle,
30 and prostate tissue cDNAs. The following RNA samples were obtained from Origene Technologies, Inc., Rockville, Maryland, and were used to synthesize the pooled driver cDNA: #HT-1015 normal colon total RNA, #HT-1005 liver total RNA, #HT-1004 spleen total RNA, #HT-1009 lung total RNA, #HT-1003 kidney total RNA,

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#HT-1006 peripheral blood leukocyte total RNA, #HT-prostate total RNA, #HM-1002 heart muscle poly A+ RNA, #HM-1007 intestine poly A+ RNA, and #HM-1008 skeletal muscle poly A+ RNA. First-strand cDNA was prepared for each using 1 microgram of RNA. A biased pool of first-strand cDNA was prepared containing
5 50% normal colon first-strand cDNA reaction and 5.56% of each of the remaining tissue first-strand cDNA reactions by volume. Eight individual amplification reactions, each containing 1 microliter of the biased first-strand cDNA reaction pool, were performed for 18 cycles. The double stranded cDNA product from all eight amplification reactions were pooled and purified for subsequent use in subtractive
10 hybridization. The colon cancer specific subtracted library was called DE and individual clones derived from this library were referred to with a number prefixed by DE.

Normalized subtracted DE colon cancer specific and pooled normal human tissue specific cDNA libraries (same as components of driver cDNA above) were
15 generated according published procedures (Daitchenko et al., 1996 PNAS 93:6025-6030, Gurskaya et al., 1996 Analytical Biochemistry 240:90-97) using Clontech Laboratories, Inc., PCR-Select cDNA subtraction kit, PT1117-1. A forty-five fold mass excess of driver cDNA (450 nanograms) was used for each subtraction experiment. Subtractive hybridization of tester with driver cDNAs was performed
20 twice, each time for about 8 -12 hours. Subtracted cancer specific DE cDNA was ligated into the pCR2.1-TOPO plasmid vector (Invitrogen Corporation, Carlsbad CA) and chemically transformed into ultracompetent Epicurian E. coli XL10-Gold cells (Stratagene, La Jolla, CA). A reverse library was also constructed wherein the tester and driver samples were switched; this library was designated as MD.

25

Construction of a normal colon specific library

This normal colon tissue specific library was made using Clontech Laboratories Inc PCR-Select kit, K1804-1, following instructions from the users manual (PT1117-1).

30 Four, 100 μ l, SMART PCR cDNA amplification reactions for each normal, non-cancerous, patient sample, were performed, starting with 1 μ l from their respective first strand cDNA reactions. Each sample was amplified for only 18 cycles using the following PCR conditions; 95 C-10 sec, 68 C 5 min. using a 9600 Perkin

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Elmer instrument. The following are Bayer Diagnostic sample identification numbers for the cDNA samples that were amplified: NPB(-) 27347, NPB(-)27859, NPB(-)28147, NPB(-)28162, NDB(-)28800, NDB(-)29243, NDB(-)29244 and NDB(-)42472. These are normal colon tissue samples obtained from the same

5 patients providing the proximal stage B MSI – and distal stage B MSI- cancer samples, which were used to prepare the DE library described above. Equal volumes of the eight normal colon cDNAs were pooled. A subtracted normal colon tissue specific library was made by subtracting the normal colon cDNA pool against a combination of pooled driver normal cDNA made from peripheral blood leukocytes

10 (PBL), liver, spleen, lung, kidney, heart, small intestine, skeletal muscle, and prostate tissue cDNAs. The following are the RNA samples that were used to synthesize the pooled driver cDNA: #HT-1005 liver total RNA, #HT-1004 spleen total RNA, #HT-1009 lung total RNA, #HT-1003 kidney total RNA, #HT-1006 peripheral blood leukocyte total RNA, #HT-prostate total RNA, #HM-1002 heart muscle poly A+

15 RNA, #HM-1007 intestine poly A+ RNA, and #HM-1008 skeletal muscle poly A+ RNA. First-strand cDNA was prepared for each using 1 microgram of RNA. A pool of first strand cDNA reactions was then made consisting of equal volumes of the nine driver tissue first-strand cDNA reactions. Eight individual amplification reactions, each containing 1 microliter of the first-strand cDNA reaction pool, were performed

20 for 18 cycles. The double stranded cDNA product from all eight amplification reactions was pooled and purified for subsequent use in subtractive hybridization. The normal colon tissue specific subtracted library was called PA and individual clones derived from this library were referred to with a number prefixed by PA.

The normalized subtracted PA normal colon specific cDNA library and a

25 subtracted normal human tissue specific cDNA library, consisting of the human tissues listed above were generated according published procedures (Daitchenko et al., 1996 PNAS 93:6025-6030, Gurskaya et al., 1996 Analytical Biochemistry 240:90-97) using Clontech Laboratories, Inc., PCR-Select cDNA subtraction kit, PT1117-1. Library construction and cloning were carried out as described above for the colon

30 cancer specific library. Out of the 1152 clones that were analyzed for differential expression, approximately 69% were differentially expressed.

Each EST isolated from each of the above libraries represents a sequence from a partial mRNA transcript, since the cDNA used for making the subtracted library

was restricted with *RsaI*, a four base cutter restriction endonuclease that generates fragments with an average size of about 600 base pairs.

Validation of differential expression in colon cancer

5 To validate that the differentially expressed sequences found in this library were specific to colon cancer, the clones were screened with cDNAs prepared from a colon cancer specific library, Delaware (DE), and a normal tissue specific library Maryland (MD).

cDNA clones were analyzed for differential expression following the procedure developed by von Stein et al., 1997, Nucleic Acids Research 25(13):2598-
10 2602 and using probes synthesized according to a published method (Jin et al., 1997, Biotechniques 23:1083-1086). Out of the 1248 clones that were analyzed for differential expression approximately 83% were differentially expressed.

Sequencing and analysis of differentially expressed clones

15 The nucleotide sequence of the inserts from clones shown to be differentially expressed was determined by single-pass sequencing from either the T7 or M13 promoter sites using fluorescently labeled dideoxynucleotides via the Sanger sequencing method. Sequences were analyzed according to methods described in the text (XI., Examples; B. Results of Public Database Search).

20 Each nucleic acid represents sequence from at least a partial mRNA transcript. The nucleic acids of the invention were assigned a sequence identification number (see attachments). The nucleic acid sequences are provided in the attached Sequence Listing.

An example of an experiment to identify differentially expressed clones is
25 shown in the Figure, "Differential Expression Analysis". The inserts from subtracted clones were amplified, electrophoresed, and blotted on to membranes as described above. The gel was hybridized with *RSAI* cut DE and MD cDNA probes as described above.

In the Figure, individual clones are designated by a number at the top of each
30 lane; the blots are aligned so that the same clone is represented in the same vertical lane in both the upper ("Cancer Probe") and lower ("Normal Probe") blot. Lanes labeled "O" indicate clones that are overexpressed, i.e., show a darker, more prominent band in the upper blot ("Cancer Probe") relative to that observed, in the

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same lane, in the lower blot ("Normal Probe"). The Lane labeled "U" indicates a clone that is underexpressed, i.e., shows a darker, more prominent band in the lower blot ("Normal Probe") relative to that observed, in the same lane, in the upper blot ("Cancer Probe"). The lane labeled "M", indicates a clone that is marginally overexpressed in cancer and normal cells.

B. Results of Public Databases Searches

The nucleotide sequence of SEQ ID Nos. 1-544 were aligned with individual sequences that were publicly available. Genbank and divisions of GenBank, such as dbEST, CGAP, and Unigene were the primary databases used to perform the sequence similarity searches. The patent database, GENESEQ, was also utilized.

A total of 544 sequences were analyzed. The sequences were first masked to identify vector-derived sequences, which were subsequently removed. The remaining sequence information was used to create the Sequence Listing (SEQ ID Nos. 1-544). Each of these sequences was used as the query sequence to perform a Blast 2 search against the databases listed above. The Blast 2 search differs from the traditional Blast search in that it allows for the introduction of gaps in order to produce an optimal alignment of two sequences.

A proprietary algorithm was developed to utilize the output from the Blast 2 searches and categorize the sequences based upon high similarity (e value < 1e-40) or identity to entries contained in the GenBank and dbEST databases. Three categories were created as follows: 1) matches to known human genes, 2) matches to human EST sequences, and 3) no significant match to either 1 or 2, and therefore a potentially novel human sequence.

Those skilled in the art will recognize, or be able to ascertain, using not more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such specific embodiments and equivalents are intended to be encompassed by the following claims.

All patents, published patent applications, and publications cited herein are incorporated by reference as if set forth fully herein.

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TABLE 1

SEQ ID NO	clone name	Tissue Probe	SEQ ID NO	clone name	Tissue Probe
1	de0020t7	U	53	de0079t7	N
2	de0041t7	N	54	de0085t7	N
3	de0056t7	U	55	de0089t7	N
4	de0064t7	N	56	de0095t7	N
5	de0092t7	U	57	de0099t7	N
6	de0142t7	N	58	de0105t7	N
7	de0153t7	M	59	de0112t7	N
8	de0163t7	U	60	de0114t7	N
9	de0188t7	N	61	de0121t7	N
10	de0190t7	U	62	de0122t7	N
11	de0201t7	M	63	de0124t7	N
12	de0225t7	U	64	de0139t7	M
13	de0246t7	U	65	de0143t7	N
14	de0257t7	N	66	de0166t7	U
15	de0285t7	O	67	de0168t7	N
16	de0529t7	U	68	de0171t7	N
17	de0629t7	U	69	de0178t7	N
18	de0727t7	O	70	de0180t7	O
19	de0787t7	U	71	de0181t7	N
20	de0810t7	N	72	de0199t7	N
21	de0833t7	N	73	de0200t7	N
22	pa0107t7	U	74	de0202t7	N
23	pa0130t7	U	75	de0205t7	N
24	pa0149t7	U	76	de0207t7	U
25	pa0185t7	U	77	de0212t7	N
26	pa0203t7	U	78	de0217t7	N
27	pa0277t7	U	79	de0220t7	U
28	pa0287t7	U	80	de0228t7	N
29	pa0293t7*	U	81	de0236t7	O
30	pa0341t7	U	82	de0243t7	N
31	pa0357t7	N	83	de0253t7	O
32	pa0361t7	U	84	de0258t7	N
33	pa0404t7	U	85	de0259t7	N
34	pa0408t7	U	86	de0262t7	N
35	pa0425t7	N	87	de0270t7	N
36	de0001t7	N	88	de0275t7	N
37	de0002t7	N	89	de0287t7	N
38	de0036t7	N	90	de0288t7	N
39	de0038t7	M	91	de0306t7	N
40	de0040t7	N	92	de0490t7	N
41	de0043t7	O	93	de0501t7	M
42	de0044t7	N	94	de0516t7	N
43	de0045t7	N	95	de0589t7	N
44	de0050t7	N	96	de0596t7	U
45	de0052t7	N	97	de0600t7	N
46	de0054t7	N	98	de0609t7	U
47	de0055t7	N	99	de0611t7	N
48	de0059t7	O	100	de0617t7	U
49	de0060t7	N	101	de0633t7	N
50	de0063t7	U	102	de0643t7	N
51	de0066t7	O	103	de0647t7	M
52	de0067t7	O	104	de0652t7	N

105	de0666t7	N	161	pa0405t7	N
106	de0695t7	U	162	pa0406t7	N
107	de0705t7	N	163	pa0409t7	U
108	de0706t7	M	164	pa0411t7	N
109	de0708t7	N	165	pa0417t7	N
110	de0724t7	N	166	pa0421t7	U
111	de0735t7	N	167	pa0429t7	U
112	de0740t7	N	168	pa0432t7	U
113	de0742t7	N	169	de0004t7	U
114	de0747t7	N	170	de0008t7	ND
115	de0764t7	N	171	de0009t7	ND
116	de0777t7	O	172	de0010t7	ND
117	de0781t7	N	173	de0011t7	ND
118	de0793t7	U	174	de0012t7	ND
119	de0794t7	N	175	de0013t7	ND
120	de0798t7	N	176	de0014t7	ND
121	de0800t7	O	177	de0016t7	ND
122	de0816t7	N	178	de0017t7	ND
123	de0818t7	N	179	de0018t7	M
124	de0835t7	N	180	de0019t7	ND
125	pa0078t7	U	181	de0023t7	O
126	pa0080t7	N	182	de0024t7	N
127	pa0088t7	U	183	de0029t7	ND
128	pa0089t7	U	184	de0030t7	ND
129	pa0095t7	U	185	de0032t7	ND
130	pa0158t7	U	186	de0033t7	O
131	pa0159t7	U	187	de0034t7	ND
132	pa0187t7	N	188	de0035t7	ND
133	pa0190t7	U	189	de0042t7	ND
134	pa0192t7	U	190	de0047t7	ND
135	pa0209t7	U	191	de0048t7	N
136	pa0215t7	N	192	de0049t7	ND
137	pa0218t7	N	193	de0051t7	O
138	pa0220t7	N	194	de0053t7	ND
139	pa0238t7	N	195	de0065t7	ND
140	pa0249t7	U	196	de0068t7	N
141	pa0256t7	N	197	de0069t7	ND
142	pa0258t7	U	198	de0071t7	N
143	pa0272t7	N	199	de0072t7	ND
144	pa0283t7	N	200	de0076t7	U
145	pa0295t7	N	201	de0077t7	ND
146	pa0309t7	U	202	de0078t7	ND
147	pa0314t7	N	203	de0080t7	ND
148	pa0317t7	N	204	de0082t7	ND
149	pa0319t7	N	205	de0086t7	ND
150	pa0323t7	N	206	de0087t7	ND
151	pa0333t7	N	207	de0088t7	ND
152	pa0336t7	N	208	de0093t7	N
153	pa0353t7	N	209	de0094t7	ND
154	pa0363t7	N	210	de0097t7	O
155	pa0364t7	N	211	de0098t7	ND
156	pa0366t7	U	212	de0100t7	ND
157	pa0382t7	N	213	de0101t7	ND
158	pa0383t7	N	214	de0102t7	ND
159	pa0388t7	N	215	de0106t7	ND
160	pa0389t7	N	216	de0109t7	U

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217	de0110t7	N	273	de0214t7	ND
218	de0111t7	N	274	de0215t7	ND
219	de0113t7	ND	275	de0218t7	ND
220	de0115t7	O	276	de0221t7	ND
221	de0117t7	ND	277	de0223t7	O
222	de0118t7	U	278	de0227t7	ND
223	de0119t7	ND	279	de0229t7	O
224	de0123t7	ND	280	de0230t7	ND
225	de0125t7	ND	281	de0232t7	ND
226	de0126t7	ND	282	de0234t7	ND
227	de0129t7	ND	283	de0235t7	ND
228	de0130t7	U	284	de0237t7	ND
229	de0131t7	O	285	de0238t7	ND
230	de0132t7	ND	286	de0239t7	N
231	de0134t7	O	287	de0241t7	N
232	de0135t7	ND	288	de0242t7	O
233	de0137t7	M	289	de0244t7	N
234	de0138t7	ND	290	de0247t7	O
235	de0140t7	ND	291	de0252t7	ND
236	de0141t7	ND	292	de0255t7	N
237	de0145t7	ND	293	de0256t7	ND
238	de0146t7	O	294	de0260t7	N
239	de0148t7	ND	295	de0261t7	N
240	de0149t7	ND	296	de0263t7	N
241	de0151t7	O	297	de0264t7	ND
242	de0152t7	ND	298	de0265t7	ND
243	de0154t7	ND	299	de0266t7	O
244	de0156t7	ND	300	de0267t7	N
245	de0157t7	U	301	de0268t7	ND
246	de0158t7	ND	302	de0272t7	ND
247	de0159t7	N	303	de0273t7	ND
248	de0162t7	ND	304	de0274t7	N
249	de0169t7	U	305	de0276t7	O
250	de0170t7	O	306	de0277t7	M
251	de0174t7	ND	307	de0279t7	N
252	de0176t7	ND	308	de0280t7	ND
253	de0177t7	O	309	de0281t7	N
254	de0182t7	ND	310	de0282t7	ND
255	de0183t7	ND	311	de0284t7	ND
256	de0184t7	ND	312	de0286t7	ND
257	de0186t7	ND	313	de0339t7	ND
258	de0187t7	M	314	de0483t7	ND
259	de0189t7	ND	315	de0484t7	M
260	de0191t7	M	316	de0491t7	ND
261	de0192t7	ND	317	de0499t7	ND
262	de0193t7	ND	318	de0507t7	M
263	de0195t7	N	319	de0511t7	O
264	de0196t7	N	320	de0519t7	ND
265	de0197t7	N	321	de0520t7	N
266	de0198t7	ND	322	de0522t7	ND
267	de0203t7	ND	323	de0524t7	M
268	de0208t7	ND	324	de0530t7	ND
269	de0209t7	N	325	de0531t7	ND
270	de0210t7	N	326	de0532t7	M
271	de0211t7	ND	327	de0534t7	N
272	de0213t7	ND	328	de0542t7	ND

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329	de0556t7	M	385	de0707t7	O
330	de0557t7	ND	386	de0709t7	O
331	de0559t7	U	387	de0710t7	ND
332	de0562t7	ND	388	de0712t7	N
333	de0566t7	U	389	de0715t7	ND
334	de0567t7	N	390	de0719t7	N
335	de0568t7	ND	391	de0722t7	ND
336	de0570t7	ND	392	de0723t7	ND
337	de0571t7	ND	393	de0725t7	N
338	de0574t7	ND	394	de0728t7	ND
339	de0581t7	ND	395	de0729t7	ND
340	de0583t7	U	396	de0731t7	ND
341	de0587t7	ND	397	de0732t7	ND
342	de0588t7	ND	398	de0737t7	ND
343	de0591t7	ND	399	de0739t7	M
344	de0592t7	ND	400	de0741t7	ND
345	de0597t7	U	401	de0744t7	N
346	de0598t7	ND	402	de0746t7	ND
347	de0599t7	ND	403	de0749t7	N
348	de0602t7	N	404	de0750t7	ND
349	de0605t7	ND	405	de0756t7	ND
350	de0608t7	ND	406	de0759t7	ND
351	de0610t7	ND	407	de0761t7	O
352	de0616t7	O	408	de0762t7	ND
353	de0619t7	U	409	de0766t7	ND
354	de0620t7	ND	410	de0768t7	U
355	de0622t7	ND	411	de0769t7	ND
356	de0623t7	ND	412	de0772t7	ND
357	de0624t7	O	413	de0776t7	ND
358	de0625t7	ND	414	de0779t7	ND
359	de0628t7	ND	415	de0785t7	ND
360	de0630t7	ND	416	de0786t7	ND
361	de0631t7	ND	417	de0788t7	ND
362	de0632t7	N	418	de0789t7	ND
363	de0634t7	ND	419	de0792t7	ND
364	de0639t7	ND	420	de0796t7	ND
365	de0642t7	ND	421	de0797t7	ND
366	de0649t7	ND	422	de0801t7	O
367	de0650t7	N	423	de0804t7	ND
368	de0656t7	N	424	de0805t7	ND
369	de0657t7	ND	425	de0806t7	ND
370	de0660t7	ND	426	de0807t7	N
371	de0661t7	O	427	de0811t7	O
372	de0662t7	O	428	de0812t7	ND
373	de0664t7	ND	429	de0817t7	N
374	de0665t7	ND	430	de0820t7	ND
375	de0667t7	ND	431	de0821t7	ND
376	de0669t7	ND	432	de0822t7	ND
377	de0676t7	ND	433	de0823t7	N
378	de0686t7	N	434	de0824t7	N
379	de0687t7	ND	435	de0825t7	ND
380	de0689t7	N	436	de0826t7	ND
381	de0691t7	M	437	de0827t7	ND
382	de0693t7	ND	438	de0829t7	ND
383	de0703t7	ND	439	de0830t7	ND
384	de0704t7	M	440	de0837t7	N

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441	de0840t7	ND
442	de0848t7	ND
443	pa0079t7	N
444	pa0081t7	ND
445	pa0082t7	ND
446	pa0083t7	ND
447	pa0084t7	ND
448	pa0085t7	ND
449	pa0086t7	M
450	pa0090t7	N
451	pa0091t7	ND
452	pa0092t7	N
453	pa0096t7	ND
454	pa0100t7	ND
455	pa0101t7	U
456	pa0103t7	ND
457	pa0104t7	ND
458	pa0114t7	ND
459	pa0115t7	ND
460	pa0118t7	ND
461	pa0120t7	ND
462	pa0129t7	ND
463	pa0131t7	U
464	pa0133t7	ND
465	pa0135t7	N
466	pa0140t7	O
467	pa0142t7	ND
468	pa0143t7	ND
469	pa0146t7	ND
470	pa0147t7	ND
471	pa0148t7	ND
472	pa0151t7	ND
473	pa0157t7	ND
474	pa0164t7	ND
475	pa0167t7	N
476	pa0171t7	U
477	pa0174t7	ND
478	pa0175t7	ND
479	pa0179t7	N
480	pa0182t7	ND
481	pa0184t7	ND
482	pa0186t7	U
483	pa0189t7	ND
484	pa0207t7	ND
485	pa0210t7	ND
486	pa0212t7	ND
487	pa0214t7	ND
488	pa0216t7	ND
489	pa0217t7	M
490	pa0219t7	N
491	pa0223t7	ND
492	pa0224t7	ND
493	pa0228t7	ND
494	pa0229t7	U
495	pa0231t7	ND
496	pa0232t7	ND

497	pa0240t7	ND
498	pa0252t7	ND
499	pa0260t7	U
500	pa0261t7	N
501	pa0262t7	ND
502	pa0264t7	N
503	pa0265t7	N
504	pa0268t7	ND
505	pa0276t7	ND
506	pa0279t7	ND
507	pa0280t7	ND
508	pa0282t7	ND
509	pa0285t7	ND
510	pa0299t7	ND
511	pa0300t7	U
512	pa0301t7	ND
513	pa0302t7	ND
514	pa0305t7	N
515	pa0306t7	ND
516	pa0307t7	ND
517	pa0311t7	ND
518	pa0316t7	ND
519	pa0318t7	ND
520	pa0321t7	M
521	pa0325t7	N
522	pa0326t7	ND
523	pa0332t7	ND
524	pa0339t7	ND
525	pa0346t7	O
526	pa0349t7	ND
527	pa0351t7	U
528	pa0355t7	ND
529	pa0358t7	ND
530	pa0360t7	N
531	pa0362t7	ND
532	pa0368t7	U
533	pa0369t7	ND
534	pa0373t7	ND
535	pa0380t7	ND
536	pa0393t7	ND
537	pa0395t7	ND
538	pa0396t7	ND
539	pa0397t7	ND
540	pa0410t7	N
541	pa0415t7	ND
542	pa0416t7	ND
543	pa0424t7	ND
544	pa0430t7	ND

* In the provisional application (60/098,639) filed August 31, 1998, clone PA0293t7 was labeled clone PA0023t7 in error. That mistake has been corrected here to reflect the accurate clone name.

Table 2

SEQ ID NO	Clone name	"Novel" Region 1		"Novel" Region 2		GenBank Identifier for top 5 matching EST sequences
		Start / Stop		Start / Stop		
36.00	de0001t7	439-607				g835668 g857149 g1321047 g1968601 g1476832
40.00	de0040t7	1-201				g2166831 g4136486 g1747976 g1180529 g2265195
41.00	de0043t7	467-615				g5129477 g1801229 g18445053 g1544683 g1694347
43.00	de0045t7	1-228				g2322205 g1139955 g4267203 g2165927 g3039227
45.00	de0052t7	455-628				g1523492 g1548890 g1523465 g1809433 g5132985
50.00	de0063t7	1-114		452-624		g2197338 g5754794 g2694448 g2070840 g3419233
51.00	de0066t7	301-631				g2162184 g749398 g1239250 g839454 g1966148
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69.00	de0178t7	485-603				g1371240 g2055704 g2208007 g1686872 g1740908
71.00	de0181t7	1-153				g1188057 g1018287 g1447796 g1025264 g1069169
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74.00	de0202t7	448-599				g2115372 g1959491 g1329334 g1198642 g1957432
75.00	de0205t7	1 to 75				g779809 g2167738 g2537620 g2656428
77.00	de0212t7	1-185				g4255939 g1548503 g1687914 g1716864 g877386
80.00	de0228t7	411-594				g3446139 g3745043 g1126367 g2163321 g1195781
82.00	de0243t7	253-604				g2001999 g1071313 g966668 g26974
83.00	de0253t7	1-133				g2111781 g1663818 g574791 g1406232 g1663812
85.00	de0259t7	241-602				g2216159 g5177204 g1969363 g1388290 g1389464
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89.00	de0287t7	364-630				g2026446 g4622337 g2021046 g2056125 g5037418
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98.00	de0609t7	434-582				g5037002 g1404408 g2816378 g759987 g2969638
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105.00	de0666i7	385-586	g2932996	g1010052	g2616680	g3277252	g2252166
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124.00	de0835i7	330-570	g2029304	g2029457	g1544689	g1947895	g2986865
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134.00	pa0192i7	444-618	g4897608	g1815096	g2051120	g3426889	g4690585
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148.00	pa0317i7	457-612	g5113829	g2080750	g3739118	g3753615	g2933157
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164.00	pa0411i7	289-345	g4810371	g2369264	g3163382	g3839554	g1950020
166.00	pa0421i7	233-745	g5747013	g4150749	g1482715	g1137706	g3900569

423-603

384-585

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TABLE 3

The following list of clones indicates those found in either the DE or PA libraries and the SW480

library

SEQ ID NO	clone name
185	de0032t7
186	de0033t7
193	de0051t7
196	de0068t7
240	de0149t7
241	de0151t7
247	de0159t7
72	de0199t7
279	de0229t7
281	de0232t7
283	de0235t7
306	de0277t7
310	de0282t7
318	de0507t7
328	de0542t7
331	de0559t7
342	de0588t7
359	de0628t7
375	de0667t7
379	de0687t7
407	de0761t7
410	de0768t7
427	de0811t7
466	pa0140t7
470	pa0147t7
481	pa0184t7
493	pa0228t7
494	pa0229t7
140	pa0249t7
506	pa0279t7
510	pa0299t7
515	pa0306t7
517	pa0311t7
518	pa0316t7
536	pa0393t7
539	pa0397t7
544	pa0430t7

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1. An isolated nucleic acid comprising a nucleotide sequence which hybridizes under stringent conditions to a sequence of SEQ ID Nos. 1-35 or a sequence complementary thereto.

2. An isolated nucleic acid comprising a nucleotide sequence at least 80% identical to a sequence corresponding to at least about 15 consecutive nucleotides of one of SEQ ID Nos. 1-35 or a sequence complementary thereto.

4. A nucleic acid according to claim 1, further comprising a transcriptional regulatory sequence operably linked to said nucleotide sequence so as to render said nucleotide sequence suitable for use as an expression vector.

20 6. A host cell transfected with the expression vector of claim 5.

8. A substantially pure nucleic acid which hybridizes under stringent conditions to a nucleic acid probe corresponding to at least 12 consecutive nucleotides of one of SEQ ID Nos. 1-168 or a sequence complementary thereto.

9. A polypeptide including an amino acid sequence encoded by a nucleic acid of claim 1 or a fragment comprising at least 25 amino acids thereof.

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10. A probe/primer comprising a substantially purified oligonucleotide, said oligonucleotide containing a region of nucleotide sequence which hybridizes under stringent conditions to at least 12 consecutive nucleotides of sense or antisense sequence selected from SEQ ID Nos. 1-168.
- 5 11. An array including at least 10 different probes of claim 10 attached to a solid support.
12. The probe/primer of claim 10, further comprising a label group attached thereto and able to be detected.
- 10 13. The probe/primer of claim 12, wherein said label group being selected from radioisotopes, fluorescent compounds, enzymes, and enzyme co-factors.
- 15 14. An antibody immunoreactive with a polypeptide of claim 9.
15. An antisense oligonucleotide analog which hybridizes under stringent conditions to at least 12 consecutive nucleotides of one of SEQ ID Nos. 1-35 or a sequence complementary thereto, and which is resistant to cleavage by a nuclelease.
- 20 16. A test kit for determining the phenotype of transformed cells, comprising the probe/primer of claim 12, for measuring a level of a nucleic acid which hybridizes under stringent conditions to a nucleic acid of SEQ ID Nos. 1-544 in a sample of cells isolated from a patient.
- 25 17. A test kit for determining the phenotype of transformed cells, comprising an antibody specific for a protein encoded by a nucleic acid which hybridizes under stringent conditions to any one of SEQ Nos. 1-544.
- 30 18. A method of determining the phenotype of a cell, comprising detecting the differential expression, relative to a normal cell, of at least one nucleic acid

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which hybridizes under stringent conditions to one of SEQ ID Nos. 1-544, wherein the nucleic acid is differentially expressed by at least a factor of two.

19. A method for determining the phenotype of cells in a sample of cells from a patient, comprising:
 - i. providing a nucleic acid probe comprising a nucleotide sequence having at least 12 consecutive nucleotides of any of SEQ ID Nos. 1-544;
 - ii. obtaining a sample of cells from a patient;
 - 10 iii. providing a second sample of cells substantially all of which are non-cancerous;
 - iv. contacting the nucleic acid probe under stringent conditions with mRNA of each of said first and second cell samples; and
 - v. comparing (a) the amount of hybridization of the probe with mRNA of the first cell sample, with (b) the amount of hybridization of the probe with mRNA of the second cell sample, wherein a difference of at least a factor of two in the amount of hybridization with the mRNA of the first cell sample as compared to the amount of hybridization with the mRNA of the second cell sample is indicative of the phenotype of cells in the first cell sample.
20. A method of determining the phenotype of a cell, comprising detecting the differential expression, relative to a normal cell, of at least one protein encoded by a nucleic acid which hybridizes under stringent conditions to one of SEQ ID Nos. 1-544, wherein the protein is differentially expressed by at least a factor of two.
21. The method of claim 20, wherein the level of said protein is detected in an immunoassay.
22. A method for determining the presence or absence of a nucleic acid which hybridizes under stringent conditions to one of SEQ ID Nos. 1-168 in a cell, comprising contacting the cell with a probe of claim 10.

23. A method for determining the presence of absence of a polypeptide encoded by a nucleic acid which hybridizes under stringent conditions to one of SEQ ID Nos. 1-35 in a cell, comprising contacting the cell with an antibody of
5 claim 14.
24. A method for detecting a mutation in a test nucleic acid which hybridizes under stringent conditions to a nucleic acid of SEQ ID Nos. 1-544 or a sequence complementary thereto, comprising
10 i. collecting a sample of cells from a patient,
ii. isolating nucleic acid from the cells of the sample,
iii. contacting the nucleic acid sample with one or more primers which specifically hybridize to a nucleic acid sequence of SEQ ID Nos. 1-544 under conditions such that hybridization and amplification of the
15 nucleic acid occurs, and
iv. comparing the presence, absence, or size of an amplification product to the amplification product of a normal cell.
25. A method for identifying an agent which alters the level of expression in a cell
20 of a nucleic acid which hybridizes under stringent conditions to one of SEQ ID Nos. 1-544 or a sequence complementary thereto, comprising
i. providing a cell;
ii. treating the cell with a test agent;
iii. determining the level of expression in the cell of a nucleic acid
25 which hybridizes under stringent conditions to one of SEQ ID Nos. 1-544 or a sequence complementary thereto; and
iv. comparing the level of expression of the nucleic acid in the treated cell with the level of expression of the nucleic acid in an untreated cell, wherein a change in the level of expression of the
30 nucleic acid in the treated cell relative to the level of expression of the nucleic acid in the untreated cell is indicative of an agent which alters the level of expression of the nucleic acid in a cell.

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26. A pharmaceutical composition comprising an agent identified by the method of claim 25.
27. A pharmaceutical composition comprising a nucleic acid which includes a nucleotide sequence which hybridizes under stringent conditions to one of SEQ ID Nos. 1-544 or a sequence complementary thereto.
28. A pharmaceutical composition comprising a polypeptide encoded by a nucleic acid which includes a nucleotide sequence that hybridizes under stringent conditions to one of SEQ ID Nos. 1-544 or a sequence complementary thereto.
29. An isolated nucleic acid comprising a portion of a nucleotide sequence of SEQ ID Nos. 36-168 or a sequence complementary thereto.
30. A gene which hybridizes to one of SEQ ID Nos. 1-35.
31. A method for detecting cancer in which one or more of SEQ ID Nos. 1-544 are used as probes, said method comprising:
 - i. collecting a sample of cells from a patient,
 - ii. isolating nucleic acid from the cells of the sample,
 - iii. contacting the nucleic acid sample with one or more primers which specifically hybridize to a nucleic acid sequence of SEQ ID Nos. 1-544 under conditions such that hybridization and amplification of the nucleic acid occurs, and
 - iv. comparing the presence, absence, or size of an amplification product to the amplification product of a normal cell.
32. A method of claim 31 in which said cancer is colon cancer.
33. A method for detecting cancer in a patient sample in which an antibody to a protein encoded by SEQ ID Nos. 1-544 is used to react with proteins in said sample.

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34. A method of claim 33 in which said cancer is colon cancer.

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Differential Expression Analysis

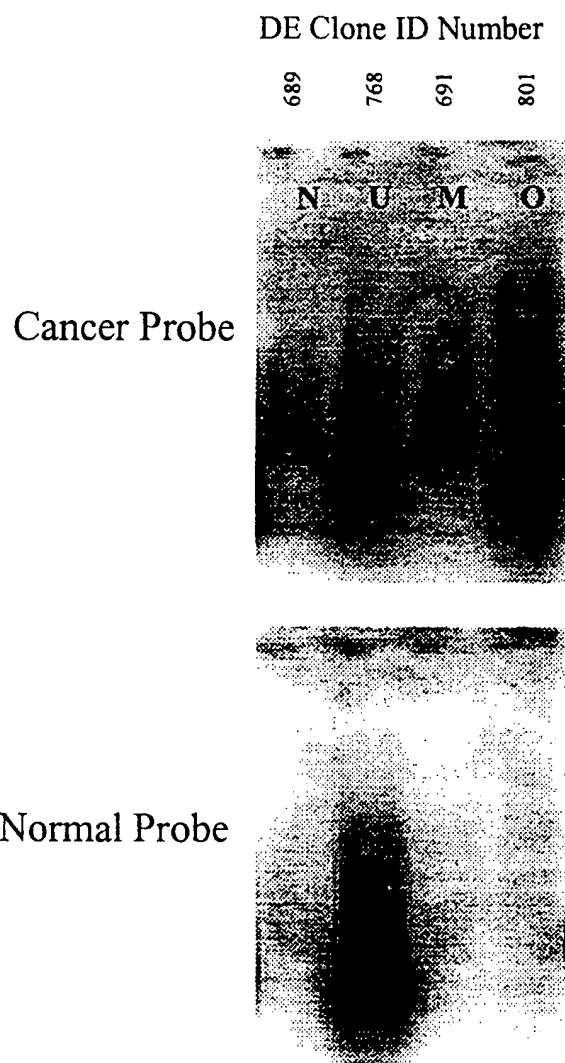


Fig. 1

SEQUENCE LISTING

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PRODUCTS: II

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cctgccaaag tgctgggatt acagggtgtg agcgatagtg ctcggcctat tatttctttt	180
taaatctttg gtagaattaa tcaactgaaac tatntgtgct ttttttgngg gaaaaattat	240
ttattttaaa gacaggggtct tgntctgttg cctgtgctgg antgcagtgg tgcaatctca	300
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ggcctnccaa acaactgggat tacaggcgtg agccctcccc tgntgatacg nagnggtttt	540
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2

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 aatatgtgta ggaatacaat tttaaagtga agattatata gatgtagata tagatagata 420
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 cttttatata tncccaaact ggtntnatgg gacctgtcct gctgtagggt aaaanccttn 540
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aagcagcctg	ggcaagagaa	gtgggtgggt	ttaggagaat	ccctttcga	aaattcagag	180
cattattatt	aatcgtttct	aaattaaatg	cagggccaag	catgctgcac	gtggaatctg	240
gacaattttt	tgataaactt	taaggctgct	aaataattta	cagaaactgt	gaatgcattt	300
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tttcataaat ctaggccaag tgacctaat gngattaaat cttaatcatc ctgngattct 540
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cccctgggta gggaaatgtg ttggaaaaga ggaactaccg ntacttctac ctcttcatec 420
tttctctttt ccctccttac aaactaaggc tttngctttc aacatcgcta tgtgggacct 480
aaaatctttg aaaattggct ttttgggaana cattgaaaga aactcctgga aactgggtcta 540
gaaagnccta attgcttctt tacacttttg nccnncnggg actgatggga tttcanactt 600
tcttgggact ttna 614

<210> 19
<211> 296
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(296)
<223> n = A,T,C or G

<400> 19
actttttttt tttttttttt ttttttttgg gatggagtct cactntgttg ccaaggetgg 60
agtgcagtgg cataatttcg gctcacttca acctctgcct cccgggttca agcaattctg 120
cgtcagcctc cggaggagct aggactacag gcatgcacca ccatgcccaa ctaatttttg 180
natttttagt agagatggag tttcaccata ttgaccagge taggctggte ttgaactcct 240
agcctnaggt gatctgcccc cctnagcccc ccaaagtacc tcggccgtga ccacgc 296

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<210> 20
<211> 565
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(565)
<223> n = A,T,C or G

<400> 20						
accaattata	atgcattatt	atgaaatatt	taaaatgggg	aatccaagat	gacatagttt	60
ttaactcatc	cacatactgg	aagtttagag	aaactcagaa	tttcttattt	ctttttcttt	120
ttcctccata	gcataaaagc	tttgctaata	agaataaata	tatatattgg	agtttttagtg	180
tttgatcctg	tgatcagttg	taaccatgtg	tcataaaact	ctctcacaga	ttccatcttt	240
cccaaattctt	ctgatcataa	cacagattgc	catatagact	tcccttgtaa	ggagaatatg	300
ctggccataa	ggcaagcana	agtgaacttg	cagtttcact	tcttggaat	taatgcattt	360
gcattgactt	ctataannta	atctctcctg	aatttttttg	cttagtcaac	ttactgtgtg	420
caaagncaac	agnaaattgt	ctttggttna	acttttaaca	ggncaattta	taaattggtt	480
tgaagaagcn	tcccnaaatt	ttttattgaa	ggctgaattc	aagcctccnt	taaaaatggnc	540
atngnataan	gggaatttat	tgtng				565

<210> 21
<211> 582
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(582)
<223> n = A,T,C or G

<400> 21						
ggtactggaa	caactataag	accctgttc	agattaagga	atttggcgca	gtttcaaaaag	60
tagacttttc	tcctcagcct	ccatataatt	atgctgtcac	agcttcctca	agaattcaca	120
tttatggccg	atactcccaa	gaacctataa	aaaccttttc	tcgatttaaa	gacacagcat	180
actgtgctac	ttttcgacaa	gatggtagat	tgcttggtgc	tggcagtga	gatggtggag	240
ttcaactttt	tgatataagt	gggagggctc	ccctcaggca	gtttgaaggc	catcaaaaagc	300
agttcataca	gtagatttta	cagctgacaa	atatcacgtg	gtctctgggg	ctgatgatta	360
tacnagttaa	atztatgggg	atattncaaa	cttccaaaga	aaattttgnc	catttaaaaag	420
aacactctng	antatggnga	aggtgnggnt	tgtgcctaac	caaacttaat	tccgggatct	480
tttttatnta	ccnggattcn	tttgatctt	ncnggtaaaa	aanggttga	tnccccaac	540
nnattgaaaa	nngttctntc	cnnttgacct	nggccanccn	ng		582

<210> 22
<211> 349
<212> DNA
<213> Homo sapiens

<400> 22						
actttttttt	tttttttttt	ttttttgaga	tggagtcttg	ctcttggtgc	ccaggctgga	60
gcaacctccg	cctcctgggt	tcaagtgatt	ctcctgcctc	aacctcccga	gtagctggga	120
ttacaggtgc	ccgccaccat	gccgagctaa	tttttgtatc	cctagtaaag	acggagtttt	180

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gccatgttgg	ccaggttggt	ctcgaactcc	taacttcatg	atctgctcac	catggcctcc	240
caaagtgtg	ggattacagg	cgtgagccac	tgtgcccaac	cctcttttcc	tttttcaa	300
gtcaatggaa	agttgattgg	aaaggacaat	ttggctacct	tttggtacc		349

<210> 23
 <211> 576
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (1)...(576)
 <223> n = A,T,C or G

<400> 23						
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tttggaactt	ttggataatg	gtgcaggcgc	tgattcttct	aagaatgatg	gagtctactc	120
caggatattt	acagcatata	cagaaaatgg	cagatatagc	ttaaaagtgc	gggctcatgg	180
aggagcaaac	actgccaggc	taaaattacg	gcctccactg	aatagagccg	cgtacatacc	240
aggctgggta	gtgaacgggg	aaattgaagc	aaacccgcc	agacctgaaa	ttgatgagga	300
tactcagacc	accttgagg	atttcagccg	aacagcatcc	ggaggtgcat	ttgtggtatc	360
acaagtccca	agccttcctt	gcctgaccaa	taccaccaa	gtcaaatcac	agacctgat	420
gccacagttc	attaggataa	gattattctt	acatggacag	caccaggaga	taattttgat	480
gttggaag	ttcaacgtta	tatcataaga	ataatgccag	tattcttgac	taagagacag	540
ttttgatgat	ctcttaagta	aatactctga	ntgccn			576

<210> 24
 <211> 618
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (1)...(618)
 <223> n = A,T,C or G

<400> 24						
acttaaaata	aagttaacaa	ttacaacaga	cccaatcaca	gacaatacca	gcgtagaaat	60
attaactcca	gaattatgac	ttttatcagg	agtaggagta	ggagtaggag	taggtgtagg	120
atcaatgtca	tcaggatttg	cttgagggat	aaacaaagt	acttgtgcaa	tggtggatac	180
ttttgatgtc	aaattgcttt	tatctatact	tttaatggca	ataaatatgt	gggttgcat	240
ttcttctgag	atattttctg	gtttaaatgc	aaagctttcc	ttggagtgg	cctccttgg	300
tgacagatca	gtagtattta	cttgaagagc	atcatcaaaa	ctgtctctta	gatcaagaat	360
acttgcactt	attcttatga	cataacgttg	aacttttcca	acatcaaaat	tatctcctgg	420
tgctgtccat	gtaagaataa	tcttatcctc	atgaactgtg	gcacaaagg	ctgtgatttg	480
acttggtggg	tattggtcag	caagggaagg	cttgggactt	gtgatccaca	aatgccctcc	540
ggatgctgtc	ggctgaaatc	ctccangtgg	ctgagtatcc	tcacaaatc	aggtcttggc	600
nggttgcttc	aattnccc					618

<210> 25
 <211> 595
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(595)
 <223> n = A,T,C or G

<400> 25
 acataccacg ctgggtagtg aacggggaaa ttgaagcaaa cccgcccaaga cctgaaattg 60
 atgaggatac tcagaccacc ttggaggatt tcagccgaac agcatccgga ggtgcatttg 120
 tggntcaca agtcccaagc cttcccttgc ctgaccaata cccaccaagt caaatcacag 180
 accttgatgc cacagntcat gaggataana ttattcttac atggacagca ccaggagata 240
 attttgatgt tggaaaagtt caacgntata tcataagaat aagtgcagt attcttgatc 300
 taagagacag ttnttatgat gctcttcaag taaatactac tgatctgtca ccaaaggagg 360
 ccaactccaa ngaaagcttt gcntttaaac cagaaaatat ctcaagaaga aatgcaaccc 420
 acatatttat tgccttnaa agtatagata nagcaatttg acatcnaagt ntccacattg 480
 nacaagnac tttggttatc cctcagcaaa tctgatgaca ttggatctac tctactctac 540
 ttctanttct gaanaaggat aatccgngt aaattttccc tggattgctg ggatg 595

<210> 26
 <211> 361
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(361)
 <223> n = A,T,C or G

<400> 26
 actttttttt tttttttttt ttttttctga gcatattata tctaattttt gaaggttgta 60
 ttttctccct tgttttaatt ttctgcanat acttttttct tttttacttt cccaattag 120
 tttgtttctg actttcttcc tcaatctctc ctgaaccatt gtttnttttt aagatcagag 180
 cagattctta ggaactttta aaactgtatg tgggtgggat tgtcacctan agtgcttttt 240
 tggagagtaa ttggatggng tgataattaa ttttatgtgt caatttgaca gggcttggg 300
 gtgtccagtt atttggttaa acattatttc tgggtgtgcc taaaagggtg tccgcgtac 360
 c 361

<210> 27
 <211> 611
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(611)
 <223> n = A,T,C or G

<400> 27
 acctgttctt ggagccaatg tgactgcttt cattgaatca cagaatggga catacagaag 60
 ttttggaaact tttggataat ggtgcaggcg ctgattcttt caagaatgat ggagtctact 120
 ccaggatatt tacagcatat acagaaaatg gcagatatag cttaaaaagt cgggctcatg 180
 gaggagcaaa cactgccagg ctaaaattac ggctccact gaatagagcc gcgtacatac 240
 caagctgggt agtgaacggg gaaattgaag caaacccgcc aagacctgaa attgatgagg 300

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<220>
<221> misc feature
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<222> (1) ... (615)

<223> n = A,T,C or G

<400> 30

ggtacagtgg	tagcatccaa	atgggcaaac	gtagtagcag	gggcagggtc	agtcaagtca	60
tcagcaggca	catagatagc	ctgtactttg	taatattctt	cccacccttg	agaatggact	120
ttgtaagatc	cgccccctgc	ccacaaaaaa	atttctccta	actccactgc	ctatcccaaa	180
cctataagaa	ctaatagataa	tcccaccacc	ctttgctgac	tctcttttca	aactcagcct	240
gcctgcgccc	aggtgattaa	aaagctttat	tgetcaccce	aagcctgttt	ggtgggtctct	300
tcacacagac	gcgcgtgaca	gaaaccactt	gaagccccggg	cgcggtggct	caggcctgta	360
atcccagcac	tttgggaggc	tgaggtgggt	ggattacctg	aggtcangag	ttcgagacca	420
gcctgaccaa	catggtaaaa	ccctgtctct	actaaaaatc	aaaaaaanta	accnngggtg	480
gtggnnngca	cctgtaattc	agttcttggg	accttangca	ngaaaatcct	tgaacttgga	540
ggcggagggtg	catanttgaa	acaaaccttg	netcaacctg	gnaacaaaat	aaaaatccgn	600
tnaaaaaana	aaaaa					615

<210> 31

<211> 485

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1) ... (485)

<223> n = A,T,C or G

<400> 31

acgcggggat	aagctacaac	ataaacacat	ctagggttctt	gttcttagaa	tacagcatga	60
agaatttgct	ttcttcttct	ttcctaacat	tttcatgtga	gatccagaaa	ggacacattg	120
tctctggcca	ttcgaagaaa	gaaagaaaga	aagaaaaaaa	aggtatttag	agacagagag	180
agaaaaaggc	tgaaatgggt	tcgctgggtt	ctaaaaatcc	gcaaaccaaa	caagcccaag	240
ttcttctttt	gggacttgac	tcagctggga	agtctactct	cctttataaa	ttaaagcttg	300
ctaaggatat	taccaccatc	cctacaatag	gtttcaatgt	ggaaatgatc	gagttggaaa	360
ggaatctttc	actcacagtc	tgggatgttg	gaggacagga	aaaaatgaga	actgtttggg	420
gctgttctgt	gagaaccnna	t'ggctngtg	tatgtgtgga	cagtccttcg	gcccgaacct	480
cttan						485

<210> 32

<211> 780

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1) ... (780)

<223> n = A,T,C or G

<400> 32

cgagggtacgc	gggtgtctag	accttatgtc	aaaataagcc	caattgtatt	aaagagtatt	60
aaattgtatt	agaataaaaa	acacatggcc	gggcacgggtg	gctcacgcct	gtaatccag	120
cactttggga	ggacgagatg	ggcggattac	aaggctcagga	gattgagacc	atcctggcta	180
acatggtgaa	accccgctc	tactaaaaat	acaaaaaaa	aattgtccag	ccgtgggtggc	240
aggtgcctct	agtccacta	ctccagagct	gaggcaggag	aatgatgtga	acccgggagg	300

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<210> 37
 <211> 245
 <212> DNA
 <213> Homo sapiens

<400> 37
 acagacatgg cggcggccttt tcggaaggcg gctaagtccc ggcagcggga acacagagag 60
 cgaagccagc ctggcctttcg aaaacatctg ggctgctgg agaaaaagaa agattacaaa 120
 cttcgtgcag atgactaccg taaaaaacaa gaatacctca aagctcttcg gaagaaggct 180
 cttgaaaaaa atccagatga attctactac aaaatgactc ggggttaaact ccaggatgga 240
 gtacc 245

<210> 38
 <211> 630
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(630)
 <223> n = A,T,C or G

<400> 38
 actacactga attcaccccc actgaaaaag atgagtatgc ctgccgtgtg aaccatgtga 60
 ctttgtcaca gcccaagata gttaagtggg atcgagacat gtaagcagca tcatggagggt 120
 ttgaagatgc cgcattttgga ttggatgaat tccaaattct gcttgcttgc tttttaatat 180
 tgatatgctt atacacttac actttatgca caaaatgtag gggtataata atgttaacat 240
 ggacatgatc ttctttataa ttctactttg agtgcgtgct ccatgtttga tgtatctgag 300
 caggttgctc cacaggtagc tctaggaggg ctggcaactt anagggtggg agcagagaat 360
 tctcttatcc aacatcaaca tcttgggtcag atttgaactc ttcaatctct ttgcactcaa 420
 agcttgttna gatagttaa gccgtgcata aattnacttc caaatttaca tactctgctt 480
 anaaattttg ggggaaaaat taaaaaatnt aattggccag gatnttggn atttgttata 540
 atgaatgaaa cattttngna ttaaaaaatca nattacttnt aanttttgat aaantaaggc 600
 atggntgggg gtaattgggt tttttgttcc 630

<210> 39
 <211> 626
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(626)
 <223> n = A,T,C or G

<400> 39
 acagtggctc ttttcagagt tggacttcta gactcacctg ttctcactcc ctgtttttaat 60
 tcaaccagc catgcaatgc caaataatag aattgctccc taccagctga acagggagga 120
 gtctgtgcag tttctgacac ttgttggtga acatggctaa atacaatggg tatcgctgag 180
 actaagtgtg agaaattaac aaatgtgctg cttgggttaa atggctacac tcatctgact 240
 cattctttat tctattttag ttggtttgta tcttgccata ggtgcgtagt ccaactcttg 300
 gtattaccct cctaatagtc atactagtag tcatactccc tgggtgtagtg tattctctaa 360

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<210> 42

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<211> 259
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(259)
<223> n = A,T,C or G

<400> 42
ngtacgggtcg gtggcagtgct tattctgaga tctgtagatg cttagaatat cagtatttttg 60
gatgttgctg cattttacaa tttatttgga gtcttccttn attttcctcc agatatatga 120
aaatatgcaa tacctgctta tatcatgtag aaaagcttag caattattaa tttttctnta 180
tttcatttta ttgacccaaa gtcgggtgctt cacttgactc antgtgtttt aggtgttngt 240
ntttntacct ttccgggtca 259

<210> 43
<211> 509
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(509)
<223> n = A,T,C or G

<400> 43
acgagtgtat ttttgatggg aaggccatgc taaatctata aaacagatgt ttcctctccc 60
aacagtggtc accagtagtt tcaacttttt cccccagta gcatcaacca aacttagcat 120
agtgtatttt aactctttgc tcccacacgc actcatccca acttccccgc ttgcccact 180
ccctgggggg aaataaccct gcctttaaaa taaatagcaa ccaagtgtct agttctatgg 240
aaagtatgaa tatttatctc aggccttcga tcccaatcga tttcaaaaaa caaagtctga 300
tttctctcct cagagcagct gaggcctcca tgttacgatg gtttcatgga gattgaagga 360
gcacatttca tcaggcttag cacaaagtcc ctgatgccca ccatgtccca gccttagnaa 420
aggaaagaaa cagaattcac caccatgggg ctgaacgaat gccacaccta atgtaaata 480
ncagctaacc ttggccaaat tgtgggttt 509

<210> 44
<211> 544
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(544)
<223> n = A,T,C or G

<400> 44
ttttttaaaa gtgtcactna ntctttaann anatncatta ccattttttt tncaaantaa 60
attacggttt taaanggaan acacatggna atntananaa ncaccgnnga annttaanta 120
cctngggngc gancanactn anggcgaatt cgaaccaatg ggggcnghnaa cnaggggatc 180
ccagctnggt accaaaattg gcgtnatgat cgcaatagcg gtacctgtgn naaanggtta 240
ttcnntngta aaancagann tcntnnaagn nngacccaaa aangtaaatc ctgggggtgcc 300

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<211> 253
 <212> DNA
 <213> Homo sapiens

<400> 47
 ggtacttttg tttgaaaaca acacttagag cctccagata acttttaaga cttattttagc 60
 tttgtgggtg gtatttttcat gcaaataagt aaggggtgggt tttatatattt gtagaagttt 120
 tcggctctat tttaatgctc tttgtatggc agtatgtata tattgtgtta agttcctcaa 180
 gaatctcctt aaaaactttg aagttaatac ttttgtgcaa ctgtgttttg aataaagcca 240
 tgacagtgtt aaa 253

<210> 48
 <211> 607
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(607)
 <223> n = A,T,C or G

<400> 48
 acttacatat cctacatttg actacattat ttccaaacca agtattccat ccaaaggaaac 60
 atactgctat catagagacc aaggagggac tgttttaaagt tgccaagggtg aagcgagctg 120
 agaggctttg tcctcgtgcc agtaactctg aaatttctct taattcctgc tgtccaggca 180
 gcagaatgcc atggtttccc caagtaggta gctgctttag cagttaaagc ccaaagtgtc 240
 gttctgttga tcaagaggtc tctgaatttc tgaagtgggt tttcgtttct ggtgactgag 300
 ttaatccttt acaatncctc ttgtaaagtg tgctaataga aagaatccac ctttcaaagc 360
 tgcagaacca naccgtgccc taaattgacc aaccgtanct gatgtgcctn angaagtctt 420
 ttgccaactg ccctgtgaan acccctnctt cccccagct ngtggcttgc acactgaaca 480
 tttaaactgn gcaaagccgt gtagttataa nacagtaa at cccaaggctt ggttaantgc 540
 tgggnnaaaa ctggttgat anacttaact taaaaccctt tacataaacn tnggaactcn 600
 aagaaaa 607

<210> 49
 <211> 421
 <212> DNA
 <213> Homo sapiens

<400> 49
 ggtaccactg gatgaggggc cgggacatac tgactgcccc tttgacccca caagaatcta 60
 tgatacagcc ttggctctct ggatcccttc tttgctcatg tctgcagggg aggctgctct 120
 atctgggttac tgctgtgtgg ctgcactcac tctacgtgga gttgggccc gcaggaagga 180
 cggacttcag gggcagctag aggaaatgac agagcttgaa tctcctaaat gtaaaaggca 240
 ggaaaatgag cagctactgg atcaaaaatca agaaatccgg gcatcacaga gaagttgggt 300
 ttaggacagg tgctgttccc gagactcagt cctaaagggt ttttttccca ctaagcaagg 360
 ggccctgacc tcgggatgag ataacaaatt gtaataaaag taacttctct tttctttcaa 420
 a 421

<210> 50
 <211> 624
 <212> DNA
 <213> Homo sapiens

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acttttaatg gtgggaattt acagtagaag catcctttgc tgagttatac attcctttat      60
caatctcttt tgatacaaca tttaaaacaa gtagcttcaa gaaaccactg gtgttttgag      120
gatagtattt ctaaatagca ttcaggaaca gagtattatt gcacagatct gaagatcaaa      180
aaaaagctca aggaaataca gatcgggaagt gctgatgagt tatattttatt gaaaacccaa      240
cttttaagga agtgctaaga tcagtcaccc atgtgaataa gaagccagga aaggaaagat      300
ggggaaagcc canatcacca ggcttctatt aaggaggaaa gcaacagang aaacagtgaa      360
agggaacaga aaggggtagc caagtgttac aaaaaanccg actggataac caaactncaa      420
aaagngtatg ttggggagaa ctgaaangga aaacaaaata cttgactaat cntaagtaga      480
aaaaagcagn tagagaaaac caaatatttc tggncctgtc acatacaact tcaaataccc      540
ttatanaatc caaaaatgat gtgtgtaagg naaaatttat tgccntccga aaaataantt      600
tntccaatnt gaaacaaatc aac                                     623

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<210> 53
<211> 627
<212> DNA
<213> Homo sapiens

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<220>
<221> misc_feature
<222> (1)...(627)
<223> n = A,T,C or G

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<400> 53
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gtgctgatcc ccaccgacaa ttcgacccca cacaaggagg atctaagcag caagattaaa      180
gaacaaaaaa ttgtgggtgga tgaactttct aaccttaaga agaataggaa agtatatagg      240
caacaacaga acagcaatat attctttctt gcagaccgaa cagaaatgct gtctgagagc      300
aagaatatat tggatgaact gaaaaaagaa taccaagaaa tagaaaactt agacaagacc      360
aaaatcaaga aatagtcacac ctgatttcac ataacaatgt gtggcatttg ttgttctgta      420
aacttttctg ctgagcattt cagtcaagat ttaaaagagg acttactata taatcttaaa      480
cagcggggac ccaatagtag taaacaattg gtaaagtctg atgttaacta ccagtgnnta      540
ttttctgntc acgtntctaca cttgangggg gtttgactac ccancctgtg gaagaagaaa      600
gaagcaatgn ggttctatgg atggaga                                     627

```

```

<210> 54
<211> 565
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(565)
<223> n = A,T,C or G

```

```

<400> 54
ttttccttga gtgctccctt ttatgtcatt ttattttctt ttatgcagac cagtgggggg      60
aaaatcccat agattcttct ggaaactgtc aagatgctgg gaagatgaat gcaaaaactta      120
catagattgg gatgtccaca gtttgattt tcaaggtatg gcttttgag gatgacgtga      180
tcaacccaaa cttctgcttg atctggtttg tctgaactc ctgccacttg ccgccaacca      240
gggcctctgc tctgatctca tacttcacca ggcgtgccgn tcgcaggctg acgtggttgt      300
gctcgtagac cgcagaggga gattccaggt ctgtgtgctt tattctctgc atgtaaaaac      360
tataagaggt agtatcatgt ttgagtcctt ttatcttaaa gaagaatcca tatagagcaa      420

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tcgtttttcga	ataagttgna	ttctctgngt	ctggcactgt	gtccagtgtc	ctcanaggat	480
gcanggggaga	anaccaaata	gtntctgagc	agtctcacat	gggaaataaa	atgtgtcccc	540
ggtaccttgg	ccgngaacac	nctaa				565

<210> 55
 <211> 451
 <212> DNA
 <213> Homo sapiens

<400> 55	
acagagatga	caagagaaaag gcacaaatga ccggagtcag ggattgtggt gagggctcca 60
catgaagaca	gcattgttga ggagaccaag ttgggaagg tgacatgtca tacatcaaaa 120
gttgcccaaa	gatagcaggt tataatgggc tagagagaaa ttagagggaa catctcttcc 180
ttcacttgaa	caacacaaa aatagaagac cagagaatag aaggatggtg acaaatccca 240
aaaaggaaat	ggaggaggag ttcgtggaag ggcagaaaca ctttaattct agagggaggg 300
tgaggcactg	ttgaaaagag aagcaaaactt tggcaggggt ggccattctg ccttgctgag 360
tcatgggctg	agatacggaa gtcactttca atcattttct acttctccca gggcactcag 420
acaaaatcag	tgcaaggtat atggaagtac c 451

<210> 56
 <211> 623
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(623)
 <223> n = A,T,C or G

<400> 56	
ggtacgcggg	gcttccgaga cgcactgggg gccggatgta gaatcctgct tatctgtgaa 60
atgcagttaa	cacatcagct ggacctatct cccgaatgca gggtaaccct tctgttattt 120
aaagatgtaa	aaaatgcggg agacttgaga agaaaggcca tgggaaggcac catcgatgga 180
tactgataa	atcctacagt gtttcaactct tgttgcccag gctggagtgc aatggcgga 240
tcttggtc	cggcaacctc tgcctcccgg gttcaagcaa ttgtcctgcc tcagcctcct 300
gagttgctgg	gattacagat tgttgatcca ttccagatac ttgtggcagc aaacaaagca 360
gttcacctct	acaaactggg aaaaatgaag acaagaactc tatctactga aattattttc 420
aacctttccc	caaataacaa tatttcagag ctttgaaaaa atttggtatc tcaacaaatg 480
acacttcaat	tctaantgnt tacattgaan aaggagagaaa acnataaatc angaatacct 540
aatatcttca	gtngaanggc atcaagggtc tcttgaaaac ttnccggaat aatgaatntn 600
ccnaagtcca	aaanattttt aac 623

<210> 57
 <211> 622
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(622)
 <223> n = A,T,C or G

<400> 57

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```

cgaggtactt tttttttttg tttttttttt tttggtttct gtcctttaat tttttaacag      60
aatatacaga gccacacaat acgatttcaa tttcaaatta tgggagatca tattcaaata      120
tgcttaggtt tgacaagttg ctgttacaat actgagaact ttcataaaaa cgggtatttaa      180
caatttttaa gataatcaaa tatctttttg ctacgtgggc caacgcatta atactaactt      240
gtttaaaaat gcagtctttt agacttcaaa ttattataaa acaatatcaa gatcatatag      300
atatacttcc tgattactca aaactcgttc cattctgatg gaggctgaag gtaaatgtta      360
ttatacatta gaacatttca tgaaaccact tctcctttgc acttacctgt aaaagtcaaa      420
aattaaacca caatttccta agacataact atttctagaa tacattgggtg taatcataaa      480
agactacnag taaattatca tttttatcta acacttttta ccacacacat ctttctctaa      540
aggaccnaaa aaaattggga atttggattc cttacataac aggactcata cttctgattt      600
aataaattnc actcttttca ag                                     622

```

```

<210> 58
<211> 471
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(471)
<223> n = A,T,C or G

```

```

<400> 58
ggtacttttt ttttgtttgt tttctagact taataaaagc ttaggattaa ttagaagaag      60
caatctagtt aaatttccca tttgtatttt attttcttga atactttttt catagttatt      120
tgtttaaaaa gatttaaaaa tcattgcact ttggtcagaa aaataataaa tatactcttat      180
aaatgtttga ttcccttcct tgctattttt attcagtaga tttttgtttg gcatcatgtt      240
gaagcaccgg aaagataaat gattttttaa aggctataga gtccaaaagg atattctttt      300
acaccaattc ttccttttaa atctcttgag gaatttgttt tcgccttact tttttttctt      360
ctgtcacaaat gctaagtggg atccgagggt cttaatatga gatttaaaat cttaaaatgn      420
ttcttatttt cagcacttac atcatttggg acctgccngg cggccgntcg a              471

```

```

<210> 59
<211> 618
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(618)
<223> n = A,T,C or G

```

```

<400> 59
ggtacatata caatcacaca actggaacaa tcaaaaccat ctatgagtgt gggtattataa      60
aaataaaatt acgttcatac aatggtagaa aatgaaatgt ttttattaat ttgattatta      120
atacaaaacc acacatatat gaattatata acctagtgtt atatatatta aaatctttat      180
gcttgcaact gaaatgtctc tactccaagg gaagtttctg atttttaatt ttcttatttt      240
aaggaatcta ttatatcac aatgattaaa atgccttaca cataggcaaa aagcagaccc      300
aatcccagca aacagaaaaa ccataagtct atcatatcac catatgtttc accatatagt      360
tttgaaaaat aatcctattt gcagtttggg atgtcttcat atttatactt attatcaaag      420
tgattgcata ttgaggcaca gagcttaag aggaaatata tattacttat aggggaacca      480
gacactgaaa caaggaatat caatcaatgg cttcaaacna aaaaaaann nnnnnnnnnn      540
nnnnnnggaa aaggaaaagt cctgncccg cggncgttca aagggcnaat tcaaccactg      600

```

ggggccgtac ttatggac

618

<210> 60
 <211> 606
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> misc_feature
 <222> (1)...(606)
 <223> n = A,T,C or G

<400> 60
 actttttaaa cctcccaac cagccctttc tcaatattca tcaaattctaa aacatttagg 60
 gggcaaaatt ctaacatggt catggatatct tgcaaatagt aaaagcttta ttctgaagga 120
 ttataaaacta gttttctcca ttttaactag cactattttg tggaaattag aaacctcttt 180
 tatttctctt cccaaaagta atacttatta taaggctgta gtatcagggt aaggatacag 240
 ataaataaag ttcacttata tcttcttaca aatgtctggg ttttaatatg gttaatcact 300
 tatatacaaa tattacaact ttttagtgca agtttttgga agaaaacttt ttgataaaac 360
 actgtgattg atgtgacttt atttttaatt taaacgatga ggtggccaga agaaagatgg 420
 gtctaaaatt tctcccatga aagatgtaaa actatggctt ttttaaaatc aaaatttcat 480
 ctttaaaata atgggttgaa atctggatng gatctgaaca gaataatcac atttaggatc 540
 tatataaatc tcaactggag tntaactgaa ggaaataccn ngattttaag aaatatnttc 600
 aaaaan 606

<210> 61
 <211> 620
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> misc_feature
 <222> (1)...(620)
 <223> n = A,T,C or G

<400> 61
 ggtacattct ggtatgaaaa catctcaaaa tgtaacaaca caagagtttg ggtcaagacg 60
 acccaccag gaggtgtgaa aaactgggtt gaactagaac tgtggaatgg aactagttta 120
 aaatatgaag cagctctaaa caccaagctt agagacattt gccctattag aaaacaaaaa 180
 tcattaaagc tacaaaataa caagtgcata catgctgaac ctgtttccag ggagtgcacat 240
 tcccttctgc caacagggtc caaactcaca cccacaaggt gtaactctct ttcctgttcc 300
 actagatttc ctttctctca tctcaaaggc cctcagaaat gacaatggaa aacgtatgaa 360
 ttgttgaaat ttaccctgtg gaccaattcc tgaagagata acagccacaa ctctgagatg 420
 attaagacat gcagtgttta cttgatgact ttctgnattt ctagaaaccc tcaaagcatt 480
 aaactgncta tttcaaaatc taaacttntc agcactttta ttatttggag taagcnnacc 540
 gaagacaatt tactggccca caggaataac cacgcttact tgtcaccata agtttacggn 600
 atggacattc actggaaaa 620

<210> 62
 <211> 614
 <212> DNA
 <213> Homo sapiens


```
<220>  
<221> misc_feature  
<222> (1)...(614)  
<223> n = A,T,C or G
```

<400> 62						
gccgaggtac	ataaatctgt	gatcccat	cttattgcac	cattcaggaa	cactttatat	60
aaatgagtgg	cttttttatt	catattatta	gtagtatcat	ggttccatta	caggccctatt	120
aacatcatac	attgtcatta	gtctttgaag	aaaaaatatg	taaatatata	tgtgtaacat	180
gagaatttct	ctctaaagca	gggcttataa	ttttttggaa	aagtttgaca	aagcatacca	240
catgaattca	gatttacctc	aagtctaaga	attatgttta	gttaggaaaa	aggaaagtca	300
ttttgacctc	aggtagaaaa	atagattgct	ttgagttt	tgtagcttta	gactttaaaa	360
agttagaatt	tattctgtaa	ctaaaaatta	tttgaaaaaa	ttatgcctct	ggtttaatta	420
ttggtgatta	cacactcttt	ctcttaccct	tgngtattga	actatgtcca	taatcaagtt	480
agtggtgagc	ctgaaaaatg	gtatgaacat	ctgatgggat	tggcacatta	ttttaaaant	540
gacatctgac	acttcaaaac	tgtcantgng	atgggttcac	cataccacgg	ntgacctnac	600
attaaatttt	nacn					614

```
<210> 63
<211> 616
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> misc_feature
<222> (1) ... (616)
<223> n = A,T,C or G
```

<400> 63						
ggtagatata	agagtaatta	gtttttattct	ctcttttttta	taaaaatcggg	tttcagatga	60
gatgttttatc	ttagactatt	ttaggggaaaa	atttttacatg	tttgagatgg	tggagtaaaa	120
agactgttaa	acattttctt	taaaaaatta	tttttacctt	acaacaatat	atttatgatg	180
tgttcagatc	aaaaatttaa	cttctgtgtc	ccagatctac	tttcaaagtg	agatttttcac	240
ttgtcagctt	aaattttctga	ctagaactaa	catttgtgta	tttttgtgct	tagtcggaat	300
acaaatttca	cagtggattt	ttgaagtttg	tccttaaatt	ggataaaaatc	aagtgtattaa	360
agttactaaa	gagataaaaa	tggttaatttc	cattttttaa	agtaatttgg	ttgtgttttat	420
agttattttgt	acttcagagtc	tcccttcacc	atttccgacg	gcatctacng	ctcaacattt	480
tttggtagcc	cangctttca	cggacttcac	gtcattattg	gctcaacttt	cctcactatc	540
tacttcaccc	gccactaata	tttcctttac	atccaacatc	ctttgacttt	naagcgcgcg	600
ctgatnctgc	attttn					616

```
<210> 64
<211> 612
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> misc_feature
<222> (1)...(612)
<223> n = A,T,C or G
```

<400> 64
ggtagacagata tcatttcttg tgtatgccat gacttgaaaa agtttgggaa gctcttttanc 60

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```

aatatcagct aanaggatat gaaatcacag gtgatagcag ttgtcattca gtaatttcct 120
acaagcagca ccccaaagga aatatagtc taatctttac tatccacttc taaatttaat 180
gtgaatttca tacatgttat tagttgtttc ctttataatt ttataaaaaat tattcatcgg 240
gagtttaact tccacttcca tgctatcgga tgtgttgggc tccatgcaag aacttggaag 300
aaaaacaggc aggaatgcat ttgcataatg acccagatca tcattttctg caactgagaa 360
ttatatttca tcattgtctc tagaagtctg caattcttta cttttctttg gtgcattatt 420
atctangtgc ccatcactgg ataatgtgga gtgactagag aagtcantta tcaactggaag 480
gncctgccc ggcggccgtt caaaaggnc antccagcan nctggcgccc gttctaattg 540
gntccaact ngggnccaan cttgngnan tcatggcnta acnngtccn ggggggaaat 600
gntntccctc ac 612

```

```

<210> C
<211> 599
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(599)
<223> n = A,T,C or G

```

```

<400> 65
acaagctaca aaatagcatc tctttcatgg tatgtttgag tgtgtaattt tagttttctt 60
tctggttgta tttgtggtag tcagatgtgt tggattgatt ccaactggac agagtaagga 120
attccagcat cctcttctg cttgctcgtt ttacccacac gatcaaacc tcaattctag 180
ttggggatgc tgtctagccc cacaccatga ctgaagcctt aagcactgtt gcgcctccat 240
gtgctttggg tcagcaaccc cagtgggtatt ctaccagagc attgtgggaa ggcagatgta 300
tagtcaggtc ccaacagcaa attgttgggt gtgagagttc taaagtatag ggggtgaagg 360
aaagagaang atatgaactc ctctgacctt aaccacattc atttaacttt tatgcctact 420
taacaagaga acctggagaa aactatcgna ttcaagagat taatcaaaat cagggtttan 480
ccagccatga ccgaaancnc cttccttaac ctcatcttgn anggctgnaa naattcannc 540
ctaggatggt taanccagaa cccngatga ttaantgtcc aaccttnatt tncatantn 599

```

```

<210> 66
<211> 611
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(611)
<223> n = A,T,C or G

```

```

<400> 66
ncatgacctt tagtggaga ttatttggtc atcaaatacc catatccaag tttccatggg 60
gcctgggaat ttcttttcac ttggatagaa agtatatatt aggaaagtcc agttaataag 120
tatttttatt taaaaaaaaa aaaaaaggaa aaaagaatca gcagaagtca agttgtctta 180
agtcttaagg ctttctggat ttcttcttgg gaggagggtc ggatcttccc aaggcctggg 240
tcctcgaata ttcttccagt catcaaactt ggagtccttg attttctcat attccgactc 300
taaagatatt ttattctctt tcagtttttt ttcaagctca ggatccattt tactcttcac 360
agcatcatat cggatttgag aaaactcacg aagacaaaaa gaaccttcaa caatcagcaa 420
caacatgggg actccatacc cagagtcttg gtcttgcgaa aagcacgcnt naaccgctgg 480
tgccaacatg agtgaactct ttcactgggt naaactccaa cnggcctacg caaactccca 540

```

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```
<210> 69
<211> 606
<212> DNA
<213> Homo sapiens
```

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<220>
<221> misc_feature
<222> (1)...(606)
<223> n = A,T,C or G

<400> 69
accaaagcat taccgcgcatg gtagagaaca cactcgcatta aaaatgttaa gctatctgaa 60
aaataaaaatg tgcaagtctt caggatggca caaaacaaag gtcaatgctt cttggggcac 120
atttcttaga gggcttgctg agtgtgtaaa tataatcgac ttttgtttgt gttacatgac 180
ttctgtgact tcattgaaaa tctgcacaat tcagtttcag ctctggatta cttcagttga 240
cctttgtgaa gggtttttatc tgtgtagaat ggggtgttga cttgttttaa cctattaaat 300
ttttattttt tttcactctg tattaanaat aaaacttact aaaagaaaag aagtttgtgt 360
tcacattaaa tgggttttgt ttggcttctt ttaatcaggg tttctgaaca ttgagatata 420
ctgaacttag agctcttcaa tcctaagaat ttcattgaaa gnctntnact ttgaacccaa 480
accanaatac ctggcgccga caccctaagg cgaattccag ccactggcng gccgtactaa 540
nggatccanc ttggtnccaa cttggggnaa catggcnaac tggttccggg gaaatggatc 600
cccnnc 606

<210> 70
<211> 611
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(611)
<223> n = A,T,C or G

<400> 70
ncgtggncgc ggccgaggtt cttttttttt tttttttttt ttttttttnn aaaangggta 60
accttaaaag tttantggcc ccccaaangn aacctggggt taatggcttc nnattttaaa 120
tttttgaaa ttaaaaaaat tacnagtttt aaatagccna tggctggnta tgttttcana 180
aaacatgatt agactaatc ttaatgggg gcttcaagct tttccttatt ggctccanaa 240
aattcacccn ctttttgncc cttcttaaaa aactggaatg ttggcatgca tttgacttca 300
cactctgaag caacatcctg acagtcaccc ncatntact caaggaatat ccgttggaat 360
acttttcana aagggaatga aagaaaggct tgatcatttt gcaaggggccc caccacgtgg 420
gcgganaaat cacttctaca gggtattacc tgganngtca aagntttctg naaaacanct 480
tgctctcaac tgggtttacca tttgggtgctg gagctnaca cgggtttaag gcccttggna 540
anggtccaag ncccaanaaa ctttcccggg ccttccggng gccttnaagg gaatccnccc 600
tgggggcgtt t 611

<210> 71
<211> 588
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(588)
<223> n = A,T,C or G

<400> 71

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```

nctgggaacn ccgaaggtgg aaggccnttt cataacattt cttgtggatc aaaccaccgg      60
gacacctttt ttncatcaa caggactagc gtcttgtcag tcttggtgac agtgacattg      120
aangtggggg cccaccgggt ctcttggtag tttcccaaga ggtcctcctc ctgagacggg      180
ctctacccat gtttaaccca aagagtgcag gccagggttcc ttatccttct gatgaaggat      240
gagagaactc atttagaagt cagagcaaac taggggtctca gtattgagaa acgcacctgc      300
canggaatc cagagacatc ggggtgcccg cgatggcctc atgaacctg cctngacggn      360
attcaggaac cctgcaaacg tgctttttga ctctattggnc agtgtgaatt ttacacaagg      420
naaacctggt cnaaggcatt ngggaattgc tccaacnnat acttcctntt aggaacccaa      480
ggaancaggt tcncgaattt tgaaaactgg gtntgaagtt ctttcttctt ttgggnacaa      540
ggccttaaca aanancttgn ggnttccaaa tggncctggc cccacacc      588

```

<210> 72

<211> 591

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(591)

<223> n = A,T,C or G

<400> 72

```

ggtacaaact tagaagaaaa ttggaagata gaaacaagat agaaaaatgaa aatattgtca      60
agagttttcag atagaaaaatg aaaaacaagc taagacaagt attggagaag tatagaagat      120
agaaaaatat aaagccaaaa attggataaa atagcactga aaaaatgagg aaattattgg      180
taaccaattt attttaaaag cccatcaatt taattttctgg tgggtgcagaa gttagaagg      240
aaagcttgag aagatgaggg tgtttacgta gaccagaacc aatttagaag aatacttgaa      300
gctagaaggg gaagttgggt aaaaatcaca tcaaaaagct actaaaagga ctggtgtaat      360
ttaaaaaaaa ctaaggcaga aggccttttg aagagttaga agaatttgga aggccttaaa      420
tatagtagct tagtttgaaa aatgtgaagg actttcgtaa cggaagtaat tcaagatcaa      480
gagtaattac ccacttaatg gttttgcctt ngacttttgg gtttaagaata tttttaaatc      540
ctgnggctnc cttaattggc cgnttgncca ngggttcenn aaatgggttc n      591

```

<210> 73

<211> 581

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(581)

<223> n = A,T,C or G

<400> 73

```

acgcgggtat ctgtaatttt tataattcat caattctgga atgctatata taatatttaa      60
aagacttttt aaatgtgttt aatttcatca tcgtaaaaag ggatcatctc agagagaaca      120
gcagtattct gcgtattttt aaaaatgctc tagagtaaca tttgaagtaa ttcactgtag      180
tgtatgccag tcctagaaat aattttttta atttctgggt tctgtttcta atacactaac      240
caagttttca aaatatattt acaaagatgc atctttaccc attattttta aatgattaag      300
gaggatagtt gcttcaggta acaagctaatt ttttcaaata ttaggccctt acagaactat      360
ttagtcaaaa agtaagatat tcctttaaaa tatataaccc aaagctttca gttaaacctat      420
gatatatcac aaatactatt aaaaaggtaa agagaaaaatg caattgcant taatgatgcc      480
caaatngtaa aatatngaga ttcaaaaagct gggnccttat ttagngggga tnccaatggn      540

```

aatgatactg gcctggnttt acctttacct tttaaaaaan a

581

<210> 74
 <211> 599
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> misc_feature
 <222> (1)...(599)
 <223> n = A,T,C or G

<400> 74
 cgaggtactt tttccgcaca tgccttgtgc ctatctgagt attgatgcca tggatgtggc 60
 cggagaacag cagctggatg tggaaacacaa cctgttcaag caacgactag ataaagatgg 120
 catccccgtg agctcagagg ctgagcggca tgagcttgyg aaagtcgagg tgacgggtgtt 180
 tgaccctgac tccctggacc ctgatcgctg tgagagctgc tatggtgctg aggcagaaga 240
 tatcaagtgc tgtaaacacct gtgaagatgt gcgggaggca tatcgcccgt anaagctggg 300
 ccttcaagaa cccagatact attgagcagt gccggcgaag agggcttcag ccagaagatg 360
 caggaaccag aagaatgaag ctgccangtg tatggctttc ttggaaagtc aaataaggtg 420
 gcccgaaact ttcactttgc ccttggggaa ganctttcca gcantcccat gtcacntcat 480
 tgacttggca aacttttgnc ttgacaaccn tnaccatgac ccactacatc ancacctgtc 540
 atttngggga ggactttcna gccttgggaa acccctngac cccccaatgg taattggcc 599

<210> 75
 <211> 594
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> misc_feature
 <222> (1)...(594)
 <223> n = A,T,C or G

<400> 75
 acatcaaatt ataaatgcaa aacaggttca gatttcatct tttgtgattt cttttaaata 60
 ctattcattt ttattttaa atgcacagtatt tccctatat tttagtcctt ccattcctag 120
 agacaaacca gttatttggg ggtgggaagt agctgaagca aagaaggaaa agtaatacct 180
 ttaacctcac tagcttcaag agtagacatt ctactagct caattttaat aattgatttt 240
 aaataggaag aaaagaggat atatttaaga tacatagaaa ttatgatgtg aagtattcat 300
 gagaatctgt agattccatc aaaataagta ggaactcatc taaaattgtt ggatttaaag 360
 aggcactttt ggttatgatt caaatatggg gaatttgaga aatattcatt ttgnccactg 420
 gatggtcact attttactaa aanggnagct ttttatgggg ggactgngac tgaggtctta 480
 aagactgaaa gaagttgggg ggttcatttt cngtaccacc ttcnnggacc atttggaact 540
 ttggccggga acaccctaa ggngnaattt cngnccctgg gggecgctca atgg 594

<210> 76
 <211> 585
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> misc_feature

<222> (1) ... (585)

<223> n = A,T,C or G

<400> 76

acgcgggggg	cggagtagca	agtggccatg	gggagcctca	gcggtctgcg	cctggtagca	60
ggaagctgtt	ttaggttatg	tgaaagagat	gtttcctcat	ctctaaggct	taccagaagc	120
tctgatttga	agagaataaa	tggattttgc	acaaaaccac	aggaaagtcc	cggagctcca	180
tcccgcactt	acaacagagt	gcctttacac	aaacctacgg	attggcagaa	aaagatcctc	240
atatggtcag	gtcgcttcaa	aaaggaagat	gaaatcccag	agactgtctc	gttggagatg	300
cttgatgctg	caaagaacaa	gatgcgagtg	aagatcagct	atctaataat	tgccctgacg	360
gtggtaggat	gcattctcat	ggttattgag	ggcaagaagg	ctgcccaga	cacgagactt	420
ttaccaagct	tgacttana	aaagaaagct	cgtcttgaaa	gangaagcnc	tntgaaggcc	480
aaaacagagt	acanaagttt	ccnngttggc	ttggattttg	aaaattcnng	aattntntat	540
aacgggcttn	tttaaaaagg	atnggnttan	gnacctttnt	taaat		585

<210> 77

<211> 591

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1) ... (591)

<223> n = A,T,C or G

<400> 77

ggtacgcggg	agtcataattt	atgaaaaaag	gtttgtgttt	tactcttgct	agtgagaaag	60
tgggacaaaa	tatacttttg	aaataaaatg	ctatatggca	cctaattatt	ttttctttta	120
aaatgcctta	agttgcagtc	tcattttgat	aatcatttgc	ttccagtgtt	taaaaattaa	180
aaaaagaatg	gggagaagg	tatgagaaga	gcattattaa	gtttccaaat	ttaatttgaa	240
ttccaaattc	acctagcaat	aaaatcta	ttttaaaaag	tatataaata	taaaatgtat	300
aatgatgga	tagatttttg	tattgatttg	caaaatgcag	attatatttg	ataggctata	360
gtatgtagat	attcctttta	ggaatattac	agctgtaaat	tatatgagac	ttgccagtca	420
aatgctattt	ggtttaaaaa	aattattgca	atctcaagtt	aatggaatat	ttttaaatcc	480
cacattcaga	gttaaaacct	ngttttcaat	gggtttttan	tgtggcactt	gnttatagat	540
taatttttaa	taacctgttn	ggaancnggg	ccttttaact	ggtccttggg	g	591

<210> 78

<211> 252

<212> DNA

<213> Homo sapiens

<400> 78

actgagaagt	attttccagt	attcgaccca	gaccagattt	caacacatgg	ttcccataca	60
ggaaggactg	ctctgcacca	ggctttatcc	aaactttata	cttggcataa	ggtgcaagg	120
aatccagagc	tgtgacgtgc	aaccgaaact	tgtgggtttt	agtgaatttt	ccaaagcagg	180
tcccagcga	caccagcttg	tcccggaaa	tattggcggc	cagcttcata	atcttctcac	240
tcacatagta	cc					252

<210> 79

<211> 571

<212> DNA

<213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1) ... (571)
 <223> n = A,T,C or G

<400> 79
 gctcgggcaa gcactttaac cttttaagcc caaccagatg agttgcctgc agttttggag 60
 gccttcagag catttcacta gacctctgtc tgtgtcgggc cagtgtcttt agccaagctt 120
 tgattaaaga tgacttcctt gtttgctcaa gaaattcgcc tttctaaaag acatgaagaa 180
 atagtatcac aaagattaat gttacttcaa caaatggaga ataaattggg tgatcaacac 240
 acagaaaagg catctcaact ccaaactgtt gagactgctt ttaaaaggaa ccttagtctt 300
 ttaaaggata tagaagcagc agaaaagtca ctacagacca ggattcacc ccttcacagg 360
 cctgaggtgg tttctcttga actcgttact gggcatcagt agaagaatat attcccaaat 420
 ngggacaagt tcttttagga agacccctta tctttttgct ggtgaaaatc aaaatgaagc 480
 nnaaaatccc ttcaaaatga ggccaacgan taactttttt aaatggcttt tcaaaaagcc 540
 ntgttaatta ancttnantg taaaggnttt t 571

<210> 80
 <211> 595
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1) ... (595)
 <223> n = A,T,C or G

<400> 80
 acctcttcct gttcgaatgg gttatccagt aaaaaagggc gtgcccatgg caaaggaggg 60
 aaatctagaa ctttttaaaga ttcccaattt tctgcatttg actcctgtag caattaaaaa 120
 gcactgtgaa gcccttaaag atttttgcac tgagtggcca gccgactgg acagtgcga 180
 gaaatgtgag aagcattttc caattgaaat tgacagcact gattatgttt catcaggacc 240
 atctgttcgg aaccccagag cacgagtagt agtctcaaga gtaaaagcttt ccagtttgaa 300
 tttgatgat cacgcaaaga agaaattaat taaacttgta ggagagcgat actgcaagac 360
 cacagatgtg cttaccatca aaacagatag gtgcccttta aggaggcaga attaccatta 420
 tgccagtgtg tctactaaca gtgttatatc atgagtcttg gaatactgaa gaatgggaaa 480
 aaagttagac tgaagccgac ttggagaatn tatatgggaa aatactatca gaaagaaata 540
 tctggnnaacc cttttccgat gaaagtgtcg anaaaatntg gaattaataa gaagn 595

<210> 81
 <211> 601
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1) ... (601)
 <223> n = A,T,C or G

<400> 81
 acgcggggga aaacaagatg gaggattcgg cctcggcctc gctgtcttct gcagccgcta 60
 ctggaacctc cacctcgact ccagcggccc cgacagcacg gaagcagctg gataaagaac 120

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<220>
<221> misc_feature
<222> (1)...(606)
<223> n = A,T,C or G
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cccann

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<220>
<221> misc_feature
<222> (1)...(613)
<223> n = A,T,C or G
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<400> 83							
gcgtggtcgg	gccgaggtac	acgttcgtca	tggcggctgg	ccctggacct	gggtaggggg		60
tccgggttca	gtggaatat	cggcggagat	gggggagcct	ccgcttggct	tctttcacac		120
gggttgcttc	ggaggaatcc	gccgtgcaaa	tctgtccgcc	cccttggcca	ctgatcccc		180
gaagagcttc	tgtcgccgct	ctaggaatac	agacattgaa	gtttgggaca	agatat ttat		240
ctaacttctg	tgtcaaaaatt	agcgacctgc	tatggcaatg	aagaaagaaa	ctgaatttgt		300
cattttcacc	tgaagaaaaa	tgatagacaa	aaatcaaacc	tgtggtgtag	gacaggattc		360
tgtgccctat	atgattttgct	gattcacata	ctcgaagaat	ggtttggtgt	ggaacanttg		420
gaggactatt	tgaatttttgc	aaactatctc	ttgnnggttt	taccaccacta	atacttttaa		480
tacttcttta	ctttactatc	tttcttctct	accttactaa	taattttctta	cacattatta		540

agaagaaaga tgttttgaaa gaagcctact ntcataatta tnggatggtn caagggaaac 600
 anggcactnt ntg 613

<210> 84
 <211> 605
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)... (605)
 <223> n = A,T,C or G

<400> 84
 ggtactatct gctgctggca aatgggggttg ctctgggtga cagggatctg ctgacccaat 60
 gctatggttt gttccagtca atgagttgag aaggctaaag ccttggttcc tatcattctt 120
 catcactaca ttggaccaca cattggcatt cagggcttgg acaattcgct ttactcctgt 180
 agattctggg aagtcatcat cctcctcagg caactcctct ggactaagtt ctaccaattc 240
 aaagccatgt ttgaggcacc attcttgagc tttttgtcgg tttataccat cttcagacac 300
 tctatcgcag accaagatca tcacctcagg taacctatgct tttgccagtg gaagccatga 360
 ggagacacta tcaaggcccg atttttgtgt gctgtcaaag taaaccacaa atgcttggac 420
 agattctgca atctctgcag taaccagaaa tttgttgggc accccacata gattgagtct 480
 gctgaaaagt atttattatc aatggncceen ggataaaaact acacattatt tggaagtact 540
 ttcncaataa gaacttnttg tccaaggtat ttttggaccn aanggnctct tgaaaaaacg 600
 gagga 605

<210> 85
 <211> 603
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)... (603)
 <223> n = A,T,C or G

<400> 85
 acagggaaatg aagactcgaa gaggagatgt cactttcctg gaagatgttt taaatgagat 60
 tcaattaagg atgctacaga acatggcttc aattaagaca actaaagaac tcaagaaccc 120
 acaagagact gcagagagyg tcgggctcgc agcactcatt attcaggact tcaaaggttt 180
 actcttatct gactacaagt tcagctggga tcgtgttttc cagagtcgcg gggacacagg 240
 tagagtaaac tgcanaagctg cctgtctgtg acttcaagg ctaggtcata aaaggagata 300
 aagcttcttc tggtctgggtg ggctgcttgc tcttgaacct tcagtctatg cacgcaacat 360
 gcctttccag ccttctgttg ttgtagagt natagaaagc aattggatca ctatngacag 420
 cggggtaaaa cttgagggaag caacctccgc cagnggtac atggagganc cctgaannaa 480
 aggaanaaaa gggcacangg gcttaatcct gtcttggaat gcttncctnt gcaatggnnc 540
 atttcaatgg ccnagccaat tatgccatcc ctgenttaan accatgggcc ttenttgnca 600
 ttn 603

<210> 86
 <211> 583
 <212> DNA
 <213> Homo sapiens

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<220>
<221> misc_feature
<222> (1)...(583)
<223> n = A,T,C or G

<400> 86
actgtaggta tttattaata atagcaatga agatgaaaga gtgatgtatc agagaggtgg 60
agataaaatc agtaaaactt agacactaaa tgatagggga aggtgyagga gaggaatgag 120
cctagaaaac ttagaatata atgggttctaa aattaaccaa agtaaggagc acaggcatta 180
gagtaggttt tgcagagaaat gaatgtttta agacacacac aggtgtctct gggacaacca 240
agaaaagtgc aacaggcaga tggattgagg agtcttcta aagataagga tttagggaact 300
gctgaattaa aattacccaa gcgtgagaag tgggtgtgtg attaaagagag aaaaaaaaaa 360
tggaggtctg aggaatacct ttaanggatt aatgaanang cccaaagggtg ggggggtggt 420
caggagtgc ccaaagttag aagtcaggga ataaacttta aagtnnggggt gtcaaaatgc 480
naatccgaaa aaaagtnagt nccttgccg gacccccag gcgaatccac ccctggngcc 540
gtctanggat ccacttgncc aacttgggaa nntggctnct ttt 583

<210> 87
<211> 332
<212> DNA
<213> Homo sapiens

<400> 87
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agcacacgtg cccactgaag tggcaccaac agaagtttgg cttgaactaa aggacatttt 120
atttttttta ctttagcaca taatttgtat atttgaaaat aatataatatt attttaccta 180
ttagattctg atttgatata caaaggacta agatattttc ttcttgaaga gacttttcga 240
ttagtccctca tatatttate tactaaaata gagtgtttac catgaacagt gtgttgcctc 300
agactattac aaagacaact ggggcaggta cc 332

<210> 88
<211> 592
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(592)
<223> n = A,T,C or G

<400> 88
cgaggtacgc ggggacaacc agctgactcc cgtagaggaa gacactgtgg aggccagttc 60
tggagctatt gcagcctcgg ttgcccggcc cgggaccgga acccgaaaaa gttatcgta 120
gaatgtcggg caaagaccga attgaaatct ttccctcgcg aatggcacag accatcatga 180
aggctcgttt aaaggagca cagacaggtc gaaacctcct gaagaaaaaa tctgatgcct 240
taactcttctg atttcgacag atcctaaaga agatnataga gactaaaatg ttgatgggcc 300
aagtgatgag agaagctgcc ttttcactag ctgaagccaa gttcacagca ggtgacttca 360
gcactacagg tattccaaat gtcaataaag cccagtgaa gattcnagcn aagaaagata 420
tgtacnagtg gtactttgnc ngtatttgaa cattccntga aggactgcng gtttttactg 480
cttgggttaa cccaagtggg gacnnnttg ttaaatataa gaggaatttt gcccaancnt 540
gggacttctg gnggaattac ttttttggaa actttttggn accttgagn aa 592

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<210> 89
<211> 630
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(630)
<223> n = A,T,C or G

```

<400> 89
acgcgggggt ctttgggccc gcgcgaacca tggccgc -at ggtggacttc caggatgagg      60
agcaggtcaa gtcctttttt gagaacatgg aggtggagtg caactaccac tgctaccacg      120
agaaggaccc ggacgggttg ttcgggctgg tggactatct ggaagggatc cgaagaatt      180
ttgatgaggc tgccaagggt ttgaagttaa actgtgaaga gaaccagcac agtgatagct      240
gctacaaact ggggggacct tatgtgactg gaaaagggtg tctgacccaa gacctgaaag      300
ctgccccagg tgctttttga tggcgtgtga gaaacctgga aagaaatcaa tagcancatg      360
tcacaacgtt ggccttctgg cacatgatgg acagggtaat gaagatggcn acctgacttt      420
ggaaaaggca aggactacta ccaaaggcct gngatggngg ntatctttca gtgcttnaaa      480
cctaattgat tttcttctag ggggcccaag ctttccaagg acatggcctt gctgtnaat      540
cttcattaaa gccttgacct ggtcatattt ggccttgcca tgcaatccat ttacttggcc      600
ggacacctan ggaatcacc actggggcgt

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<210> 90
<211> 653
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(653)
<223> n = A,T,C or G

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<400> 90
ggtaccactt cactccagcc tggcgacaga gtggaactcc gtctcaaaaa ataaaataaa      60
ataaaaataa gcaaaaatat aaaatgttaa aaaaaaaaca aaaaaaggga aaaaggaagc      120
tgattgcctt ggtgagtcaa cactgggtat tttctgacca ctatttgaaa caaaaaagga      180
aaccactgat attctatgca aagatctgtt cctggaaggc actctgcgga gacaccagga      240
gaacttttat caatccttca ttgatttgaa gtaaaagtgc taaagcaatg gttggtgggt      300
ggcaaccat tagcagatca caaaatcact gtagtgggta actaaacaag aggaaacaca      360
agacggcatc ctgtgtaact ggggttaagc attactctct gaaactcatg gcatcagttt      420
cctcttaggc tcttcccaca aagtataatc atgttcattt cagtttacia tcccttgag      480
tcccatcgat ttgtgagaa atcccaagtc atnccacagng gagnctggaa atggctentan      540
ttgtctgcc cggcngcgt tcnaanggcg aattcaacac actggcngcc gttctaattg      600
atccaaactc naccaacctg gnggaacatg gctactgggt ctgngnnaaa tgn      653

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<210> 91
<211> 657
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature

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<222> (1)...(657)

<223> n = A,T,C or G

<400> 91

actttttttt	ttttttttt	ttttttttt	ggagaaaagc	ctnactccgt	tgccccaggt	60
ggagtgcagt	ggcgtggnc	tagcttattg	catgcagcct	naacctccca	ggctnaagca	120
atnctccnac	ctnnnctgc	tgnnttnntg	gaactacnca	tncacnccat	tatgcccanc	180
tngtngttgt	naatttaaag	tganaccatg	cncncagggn	gnatggcctt	nnntancnan	240
catgcagtgt	cagctgtgtg	gtgcacgcac	aggataaatg	gaagggggat	ttgatcaggg	300
tttttgtcac	atnagcattn	naaatccgna	ngactgcctt	gtgtctgctt	ttgnaagggc	360
ctgggagtat	tctgtgtagc	ctttgnaaat	aagggnaaaa	tgngcncctg	ccaaagaagt	420
cnttgctact	ntgggtgngt	caaaatntcc	ctgtaacttg	tcaatggnc	caagcttggn	480
ggngtntttg	ggntcttggn	tgtcnttttn	acgtctattg	nccatgtggg	tcttatatga	540
cacantcctc	ntnataatcc	ntganaattg	ctaanttgc	cttttttttt	tttttnanatt	600
nattttgctn	ttaaantagc	ttaanncttt	ntttatcctn	gggcancnca	anncaat	657

<210> 92

<211> 653

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(653)

<223> n = A,T,C or G

<400> 92

accataaaac	cattaaaagc	aataaataac	tagagtcagt	tgagatgttt	caaagactgc	60
tggaggtttc	tgtaaaccag	ggtaatcaga	aatattaccc	ttgtagatag	ccctctcata	120
ccagtaaata	caaagagtta	aaattccaat	gccacagtgt	aacagttaac	aatctatttt	180
gtaattttta	atattactac	attaattcac	cctgagaata	cagaggaaac	atttaataca	240
agacattctg	atatgntttt	ttttccatt	gnatttgctt	tcttctggnt	ttcatcagcc	300
ctttaagggc	acagatattt	taatttaaag	ggtgatttgg	atatgctttt	ttggtaactg	360
agatttatgc	cacagtcaga	tactggtgat	agaaaagccc	aaaaaggntt	gnagaaaaga	420
ggcaagcagc	aatccccagg	cagaaaagac	ngaaagtctt	gaaaaagaag	aggagtaaaa	480
atttttttta	gctgntcaat	gcctgtatt	tgggnacaag	tacctttatt	ttccttttagc	540
tganggnant	cagagtaacc	gaattgggag	nnnactattt	tcnctggnaa	ggaaaataga	600
atttggnaat	ccnggaang	gtncnngaaa	tnnagcccca	tccatttggn	gng	653

<210> 93

<211> 640

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(640)

<223> n = A,T,C or G

<400> 93

acagagaaac	cacagggtgc	cctttccaca	gctggataga	cttatccaaa	acggcaggat	60
ggttctgtat	taatcttttt	ggaaagcatg	tctgtattaa	gattgcaaaa	catacagata	120
gctaccacaa	attaggtcaa	acgactgatc	aagttgtaac	atctgtgagg	tcaaattcca	180

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$\langle 210 \rangle$	96
$\langle 211 \rangle$	655

<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(655)
<223> n = A,T,C or G

<400> 96
 ggtacaggtt tttatgtgaa catacatttt catttttctgg gataaatgct caaaagggca 60
 actgttgggt tgtatggtaa acacatatat ttttgtaaga aactacccta ctctttttcc 120
 agagtggctc tactttttac atacagccac tcatacaatt cagacagcaa tgtatgattg 180
 atccagtttc ttcacatcct caccagcatt tgggtattact actatttttt atcttaacca 240
 ttcacataga tgtgtgtaat gataccacat gtgggttttaa tttgcatttc caatggctaa 300
 tgatgttgag tatctttttg tgtgctaatt tgccatctat gtatcctctt cggtgaaatg 360
 tcttcatgtc ttttgnctat tttctattta agncatttgg tctttttact attgagtttg 420
 agagggtttt tatatatcct agataaaaat cctctgggtan anatgtgggt gcctggaatt 480
 ttaacataac ttctacccan ggaaaaataag taaaatttcc acccttgctg gcnagcctta 540
 cttaatnccg gccttaangg tccttctaga gaattaagaa gatttgaggt ttaaatanaa 600
 tcagggcntt aaaaagtaat cctaaaaatcn ggtttaagca agccatatcc tgggg 655

<210> 97
<211> 224
<212> DNA
<213> Homo sapiens

<400> 97
 acaagtttaa ggtaggacgc agcattttat agtgttacgt ccttctctcc cacatttctg 60
 tgaggcgga caagaacaat tacttgaccc tggaggaaga cgacgccttg tggtcaggga 120
 gagaacagca gttcatgctg gctgcctcgt ctttccaggc ctgctgctgc ccaggcttct 180
 actgaccttg ttaggtctga ttctagaaaa tgaaggcagg tacc 224

<210> 98
<211> 582
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(582)
<223> n = A,T,C or G

<400> 98
 ggtaccacca tgccctgggtt attgttttat ttttttggca gagatgggtc tcaactgtgtt 60
 gccaggctg atctcaaact cctggcctca agcgatctc ccatctcage ctcccaaagt 120
 gctgggatta cagacctgag ccaccacacc tgggcaacag agtgaaacct gtccctgttt 180
 tctgtctctt actctcacct ctgaggcctc ctctgcctgg aagagattac agggaaattc 240
 caggcagccc ttgtcaattg tttttatgaa ttctttacct gttcctttta aagacaagga 300
 aactgaggcc caaagtctta agttgttttg caaatggagt ctctaccct cagctcctgc 360
 aaggacctgg gggaccccca ggtccagcag ccacatgatt ctgcacagac agggacctag 420
 agcacatctg gatttaagcc caccctggca actggctgct agagactncc aagatgccga 480
 taataggatc tgcctntaaa aaatctggat tctggcctgc ntaantgcta cttcatttgg 540
 ctacaaagnt ttaaggngga acctntaaaa ccttcccaaa aa 582

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<210> 99
<211> 619
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(619)
<223> n = A,T,C or G

<400> 99
ggtacagtgg tctttttcag agttggactt ctagactcac ctgtttctcac tccctgtttt 60
aattcaaccc agccatgcaa tgccaaataa tagaattgct ccctaccagc tgaacagggg 120
ggagtctgtg cagtttctga cacttggtgt tgaacatggc taaatacaat gggatcgct 180
gagactaagt tgtagaaatt aacaaatgtg ctgcttggtt aaaatggcta cactcatctg 240
actcattctt tattctattt tagttgggtt gtatcttgcc taagggtgct agtccaactc 300
ttgggtattac cctcctaata gtcatactag tagtcatact ccttggtgta gtgtattctc 360
taaaagcttt aaatgtctgc atgcagccag ccatcaaata gtgaatgggc tctctttggc 420
tggaattaca aaactcagag aaaatgtgcc catcangaga acatcataac ccatggaagg 480
atnaaagccc caaatggngg naactgataa tagccctaata ggctttaaga atttggggcac 540
actnttacct agnggaaccc atttgancn anggggctta aaggcttntt acttcaactg 600
aaagttnagg gaaaaaaan 619

<210> 100
<211> 614
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(614)
<223> n = A,T,C or G

<400> 100
acgcggggga agcaaaggag agggaagctg gaagcacctt tggcccgga cagaaatctg 60
gagagcttgg ctacctccat cctcctcagg ccggagcagg cttcctgaga gaggccagg 120
cgtaggagtt ttacgactta gaaaagcggg ctgcagattc cttcctgggt gtttggttca 180
agccctggct ccagcctcac tctcagtctt cccgggagtt cgtgggattt ggaccttaga 240
ttattagtat tattttgagg gctcctgtg tgtaagcact ggttggtgct agatggctgt 300
gcagagggcc atgaggtaga ggctggggaa atgagggctt ggagggtgct gaggatatgt 360
ctttacctac gtgaaatgtt ggagggttag atgaaaactc ttgctttgaa atcttcatgg 420
aggactacat catttcaatc ctgaatctgg cccaattcta ttaatcactt aatacctgga 480
ttaaaaaacg nttaantggg ccaggcncaa tgggtcacgc ctgnaatccc agccttttgg 540
gaggccaagg cangccgat acnttagggc ngnanttnaa accancttgg caaattggga 600
aaccgcgntt tntn 614

<210> 101
<211> 625
<212> DNA
<213> Homo sapiens

<220>

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<221> misc_feature
<222> (1)...(625)
<223> n = A,T,C or G

<400> 101
 ggtactttgc ctacggcagc aacctgctga cagagaggat ccacctccga aacccctcgg 60
 cggcggttctt ctgtgtggcc cgcctgcagg caagaagggg ttaaaagtgg aatgtatggt 120
 gtaatagaag ttaaagtgtg gactcaagaa ggaaaagaaa taacctgtcg aagtatatctg 180
 atgacaaatt acgaaagtgc tcccnatcc ccacagtata aaaagattat ttgcatgggt 240
 gcaaaagaaa atggtttgccc gntggagtat caagagaagt taaaagcaat agaaccacaaat 300
 gactatacag gaaaggtctc agaagaaatt gaaagacatc atcaaaaagg ggnaaacaca 360
 aactcttttag aaccatanen gaatatatct taagggtttt cctatgtgcc taatataata 420
 tatttttaac acttgagaac cagggatttt gggggattct ccaacgtttg ttcaatttta 480
 agaantgggt tgaaggagtt ttttacttgg gtnattcntg gttttaggat tttnnannngn 540
 aanntggntt ngnggtttgn nnttttaann gggntntttt ngggtcttna aatttttcca 600
 anaaanngtg gnttccttcc cggnn 625

<210> 102
<211> 605
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(605)
<223> n = A,T,C or G

<400> 102
 ggtacaagaa agaaaaaata taaaaacaag tctgctgagt gtcgggagtt ggtgagggat 60
 atcctaccat attgtgacgg agtccaaata gaaaacatgc agcaacagtt ctccctgcttt 120
 atcagctccc tggaaaataa accagtaacc ctggtagtgc agtaaccatt tgggtaacag 180
 gacaaacttc ctgatggaca cagatagtaa ttcactgcat tcccttctc taacttctct 240
 ctccacacca attccttttc tttcctttta gatgggtttc atcctgttga caaaagattt 300
 ggttttattt gtaaagttaa gcagataata tcttgattga agtattcaat gatttaattg 360
 aggatgcttg gggatcaaac tttgtaaaaa ggtcaattaa gctagttagc agagactatc 420
 agtggcttgc agaaaaaaa ntcngatata tgggttggtg aaangcccaa aggataaccg 480
 ngaaaaatcc tanggatacc gggacctaataaat caaagc canaggggga ccttggttaa 540
 anccnttact tnggggangg gctnaanggn ggntccaaac naaattgggt cccaacgggc 600
 ccggg 605

<210> 103
<211> 251
<212> DNA
<213> Homo sapiens

<400> 103
 acgcgggatt ttacattcca tcttttctga agattgtcct acaatttgga ttttgatcat 60
 gacaaagaag attaaaattt cattagcatg aatgcaattt gttaaagcag actgatttgt 120
 ttctaagata tttttggtt ttttaaaact gataataatg ctgaattatc ttaagtgaga 180
 tgtaagccc actttgttct ttaatgtaa tggagcttat gggtagaaga ccatgtctac 240
 taattacaaa a 251

<210> 104

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<211> 293
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(293)
<223> n = A,T,C or G

<400> 104
ttaatcttgc acaaattggca ttttattaaa gaaaatctaa tttacaaagc tttgtaaatt 60
ttaagaaaaa c^+tcataga tcataaacia aaatttcaat atgcaatatt caaattttaca 120
agaaaataag cacaaacttt tagacagtgc agttattgct gcactccttt aattcctttat 180
ccagagccca aaaaatgtag acaaacccta aaaatgtagc agaagcattt ccgcacactg 240
gtgtccagaa tctagtgtgt gcanaaatgt ttccactaga tttatagagt acc 293

<210> 105
<211> 586
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(586)
<223> n = A,T,C or G

<400> 105
acatcatttc tgccatgttg gacattttct tgggaatata caagtaatac tccatgtagc 60
ctgacaggtc ctcaatgggt acatcatcca cgaagactcg agcttgctca gaacaggatc 120
ggggagagcc agacagagtt ctggcggtgca gcgactgaga gtagtcctca agtgtggatc 180
ttcgttcttg agccaaggga gggacactct gcgggcctga aaaggaatac acttccatat 240
catgccatct cttacactgg cattccttgc ctatgcatgt gcatggcttg ccttggttta 300
gcttggaac tgattgaaag tcagagagat cactggcttt gagacttgct tgggggactt 360
gggtagccgt cagaggagtc ttcttcttta ctctctgatg ggagccttgg aacagaaaagt 420
tctcaaangc tnaacgactg gccctggggt gaatagcatc gagagaagta naccttcttc 480
ctgnactgaa ctnttaaggg gatgaaatc ccagccaatg gtggccttan gnnangcaan 540
ntggcctttg gcttgaatta ctggntggaa aaaacctttg gccntt 586

<210> 106
<211> 644
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(644)
<223> n = A,T,C or G

<400> 106
ggtacnttga ttgctcanat ataangaaat ggcccaatga acgtggntgn gggaggggaa 60
anangaaaca gagctagnca tatgtgaatt gntctgtggn ataaacatgt taaaacanac 120
aaanatggnt atttttcttt ncttcggac agtgcacatt atcatntgaa ctacctgggg 180
attctntatc anaactgggt ttgttgaata tttatactta attgaaataa ttccttanng 240

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<210> 109
 <211> 317
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1) ... (317)
 <223> n = A,T,C or G

<400> 109
 tttgtatttt tagtagaggc agtggtttcac cgtgttagcc aggatggctt cgatctcctg 60
 acctcgtgat ccacccacct cgacctccca aagtgcctggg attacaggcg tgagccacca 120
 cgcccggcct cttttttttt tagctgccaa tctttttgaa ggaatattct tacctctact 180
 ttgtcacctt ctactggctc cttaactaaa atctgccatt tggctctctg gttaacagtc 240
 ccttcctgta aagtctaaaa tcttaattct aaatccacag ttttaattcac aagctagtag 300
 cttggccgng accacgc 317

<210> 110
 <211> 603
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1) ... (603)
 <223> n = A,T,C or G

<400> 110
 ggtacattca ggatccctcg gcccaaggact ggaccagaag aacacttggg aatcttgggt 60
 ccacttatca aaggtgaagt tggatgatc ctgactgtgg tattcaagaa taatgccagc 120
 cgcccctact ctgtgcatgc tcatggagtg ctagaatcta ctactgtctg gccactggct 180
 gctgagcctg gtgagggtgt cacttatcag tggaaacatcc cagagaggtc tggccctggg 240
 cccaatgact ctgcttggtc ttcttggtc tattattctg cagtggatcc catcaaggac 300
 atgtatagtg gcctgggtgg gcccttggct atctgccaaa agggcatcct ggaaccccat 360
 ggaagaccga gtgacctgga tcnngaattt gcattgggtg tcctgaattt tgatgaaaat 420
 aancctggna tttggaagga aatgtgcaac catgggtcca agaatccagc cnnattacc 480
 taccggatga accttnttg gaaaccataa aatgcctgca atcaatggga actttttcca 540
 accttanggg cttaccatga ccttgcccgg cgggcnttt aaanggccaa ttccaccacc 600
 tgg 603

<210> 111
 <211> 595
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1) ... (595)
 <223> n = A,T,C or G

<400> 111

```

acattttaagt tcccatgtta cagaatccca tattgtgact atttccctcaa aactaactgc      60
tagtaaagaa ccattcttcgg agaaacaaca gttagttgct tgatacttgt gataactacc      120
aacaaagtca caggtccagc caacagcttt tttgtatatg tcagagtcac ctgttaatat      180
ccatactttg aagtaaccat ctttgcctagc tgtaaccaag gtgggctgtt cagatttttc      240
tgcattacag aaacagagag ctgtaatgca gtcttcgtgt ggcattgttaa ttttagtggt      300
aagaataaac ccttgtgttt tcttattata catccacagt ttcatttgca attcaagctc      360
aagtttcctt ttcttgccgc tggccactg gtgcaagcca gttaccaaag cagccaatgc      420
aagccttggg aagtcatttt ggatcaganc ataatacanta atatatcctg ctggataata      480
ctaaattgga tactggntat cactntggag agaataaact gcaggtggcn ggntttcatt      540
caaaccaagc ttttagtcttg gacaatcatn aaccagnгаа atactcctat ntttn      595

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<210> 112
 <211> 523
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(523)
 <223> n = A,T,C or G

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<400> 112
acaagagcta ttagagatgc tgccatatgg atgggcaaaa ctgagccaat cccacttagg      60
aatggaaggc ttggacatgg aaggaggat ataaacgagg agttggagaa aaacgcaagc      120
ccagtttttg cttagagtga aatgaaagtg ggaatgaggg tcttgttttt agtcctctaa      180
ggaccaggaa gcaattttaa aacttccttg gtttttctga aagcagcata ttcaaaatgc      240
cagcaaaaac tcctaacaac tgcaaaacca aaagaggatc aaagctcacc aacatccctt      300
cttattgctg aaaggctcta aaattcagga tgcctgtttc ccttgtaaaa gggaaaataa      360
ttaaagtctg atttatggta atcataccac atcacacttc taaaaaataa tttcaagtgt      420
gtgaccaggg gaccgtttga ccnccatttt attaaccttc actttantgg gaaaaataaa      480
accttttcca gggccatttn atnccaggac ttttagtagg ggg      523

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<210> 113
 <211> 578
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(578)
 <223> n = A,T,C or G

```

<400> 113
acagtgtaaa taactaagtt gttaactgtc aagtcagtt atgtattctg taagttgtgt      60
tctagtcttt gactaaaatt tatcatctct tataatggga cttaatcttt ctctaaaagc      120
atataagagc ttgtcaatag agcaatcaat caaaaagatt ttgtgattca taacattgaa      180
gttagtctgg ttaagagttt tggtttagac ttcatttata ttttccttac taatatctaa      240
tatttaatga ataatgatca attttttata aagttattaa tatgatcagg gaaacctttg      300
ggacttctga caggcatctg gtgaagagac aattcaagcc ttagtgacta tttagaatag      360
ccagtgatca ctagtcaatt ctcatatcca tgcccttttt gccctgggta cagtcttaaa      420
agaggtaaaa cagcaaatat tttttttaag ggaactataa ccctangaat tcttgaaaag      480
aatttcaaaa aaaataagac cctgtggcca tggngnccaa acntaagacc tactatggct      540
atattgggtcc attaaaaata aattactact aatccaaa      578

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<210> 114
<211> 613
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(613)
<223> n = A,T,C or G

<400> 114
acggtagtaa gaaacctttg agatctttct gactt...caa aattagagaa agcaaattggg 60
atggatagat tttttttttc ttttcaaggg gggcaggaag gtaattggtt gagtagcctt 120
tgtttaaaaa aaaactaaat atatttaaaa ggccacattt atattttttt cacaagaacc 180
acataataaa ttccacttct tgacctgaat ttggaaatcc gaaattacta atccaggcca 240
ggtgtgggtg ctcattgcctg taatcccagc actttgagag gccgaggtgg gcagatcact 300
tgaggcctgg agttcaagac caccttggcg aacacgggtga aaccccgctc ctacgaaaaa 360
aaaaanatat aaaaaaagta ctggttatta accaaccagc ttagaaaaat aatcatggtn 420
gacacnttan ttcattcttc taaaagcctg ttgatctggg ccttcctgtt gccagcatti 480
cccttttttc aaaaatgggg ggctttttct ttaattnnac ctctgtggngn aananaattt 540
gaagggcccc aggaagtntt ttgggcnctt tgaagcgttt tncacnctn tagattctnt 600
gattaaatcc tcc 613

<210> 115
<211> 190
<212> DNA
<213> Homo sapiens

<400> 115
ggtacattgc cactgagtaa agagtggcac cagccacggt ggtagggtgga agaaacatag 60
atcccaatga ggacacaaag acgagaccca ggcccactcc caggggtgca cccatgttca 120
gaaacttttc actgggcgca cacatggcca cagtggagag gcctcccaca atgccagctg 180
tgtacttttt 190

<210> 116
<211> 610
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(610)
<223> n = A,T,C or G

<400> 116
ggtactcttg gtttatcaat gggacgttcc agcaatccac acaagagctc tttatcccca 60
acatcactgt gaataatagc ggatcctata tgtgccaaag ccataactca gccactggcc 120
tcaataggac cacagtcacg atgatcacag tctctggaag tgctcctgtc ctctcagctg 180
tgggccaccg cggcatcacg attggagtgc tggccagggt ggctctgata tagcagccct 240
ggtgtatttt cgatatttca ggaagactgg cagattggac cagaccctga attcttctag 300
ctcctncaat cccattttat cccatggaac cactaaaaac aaggtctgct ctgctcctga 360
gccctatatg ctggagatgg acaactcaat gaaaatttaa agggaaaacc cttangcctg 420

```

aagggtgtgtg ccacttcaga gactttacct taacttgaga cngntcaaac ttgcaaacca      480
tggngngggaa atttgccgaa cttttacactt tgggcagggtt ttttccaga agtcanaaca      540
agaactcctn ntcttganaa ggggtttanc ccctttnaat ggccttgctt atgctgcctt      600
tttcggttg      610

```

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<210> 117
<211> 608
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(608)
<223> n = A,T,C or G

```

```

<400> 117
ggtacgcggg ggggtattatt tgtgccaaacc aatgatgctt ttaaggggaat gactagtga      60
gaaaaagaaa ttctgatacg ggacaaaaat gctcttcaaa acatcattct ttatcacctg      120
acaccaggag ttttcattgg aaaaggattt gaacctgggtg ttactaacat tttaaagacc      180
acacaaggaa gcaaaatctt tctgaaagaa gtaaatgata cacttctggt gaatgaattg      240
aatcaaaaag aatctgacat catgacaaca aatgggtgtaa ttcattgttg agataaactc      300
ctctatccag cagacacacc tgttggaat gatcaactgc tggaaatact taataaatta      360
atcaaatcat ccaaatthaag tttgttcgtg gtagcacctt caaagaaaat ccccgtagct      420
gctatagacc cacactaacc aaagggtcaaa attgaaaggt gacctgaatt cagactggat      480
taaagaaagg tgaaccatt actgaaagt gatncatggg gaagccattt tttaaaaaat      540
nccccaaanc attgatggga attccttnng gaaatacttg aaaggaaccn nnnnagacca      600
atcnttcc      608

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<210> 118
<211> 578
<212> DNA
<213> Homo sapiens

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<220>
<221> misc_feature
<222> (1)...(578)
<223> n = A,T,C or G

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<400> 118
actccactta gcaaatgccc tgccagcaaa gtcacagatg actttttttac ccaatcttag      60
gtaaatctgg attatctgcc caaccgtgca agtcaataag ccacccttga aaactgtgtc      120
aagatttgag gaaacaggtc ttaagaacct atccaacaca tgattccata accaatatcat      180
cttangttgt tttaggcaaa taagtgtatc tcttgaatca ctgatggatt caatatcaag      240
atctataatt ttcacgttta aaattttactc tgccgaggac attttatttg taaagcataa      300
accagttagt ttgacagaca cnaaaaagaa aacnaaatgt tcacagtcct atcttcgtag      360
ggatttcttg ctataaaaaat tggcttcagg ttcaaggctc tagaccactc ttctaaggct      420
nctactggat atantantta ccacttgggg nccaaactta aaacctcntg gactttttcc      480
ccttanggac nangaaaaac caaggggttg tggtttgaac tcctacact tggngnnaaa      540
ncttttcttg gnngnatnta aanattaagg ggcttttn      578

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<210> 119
<211> 584
<212> DNA

```

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(584)

<223> n = A,T,C or G

<400> 119

actgtcttag	aatattat	at	ttttttgt	at	ttgtaaat	ctgtggacaa	aagagggttt	60
cctcactcct	tttactcact	gg	gtcatga	cag	tgaagga	gatgctccat	ctgcttctcc	120
ccctttctct	tgctgtagtc	caat	gtgcta	tgag	catcag	cttactttgc	cacttagagc	180
aagcaaaacc	cagtgcaga	gtct	cggtca	gctcta	aaata	ggtttgcttt	cttttagtta	240
cagtgcccat	tttgaaattg	cctata	cagt	cttag	tgacc	at	ttaaaccg	300
gcgtttaatt	ttcacttctt	catgt	ttnaat	tngcag	ttca	anatttatag	naagatggnt	360
atttcgaaaa	nacaaaaaan	tggn	ttttta	anaaaa	anaag	tncnttggtc	ggcgaancan	420
gcntaagggg	cgaatttcca	gcnca	actgg	gcngg	cccg	nncntagnng	atccccaacc	480
tttggtaccc	angcttnggc	nntaan	caat	tggncc	anag	nttgtttccc	tggggtgaaa	540
antngtnatc	ccgttcccaa	ttcccn	naca	ncnnacc	nnng	cccc		584

<210> 120

<211> 587

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(587)

<223> n = A,T,C or G

<400> 120

acgcgggggc	cgtagcagcc	gccgcccac	cctctttgtg	tgctttggaa	agccgcggag	60
ctggtggtgg	ctacagttgg	tggtgggggc	ttaggcgagg	gacgttaccg	ggaagttgca	120
ggcgggagga	ctcttcccca	tccagtcacc	tgacaggtca	caaacatgtc	agacaaaagt	180
gaattaaaagg	ctgagttgga	acgtaagaag	cagcgactgg	cccaaatcag	agaggaaaag	240
aagagaaaag	aagangaagg	gaaaaaaaaa	gaaacagacc	anaataagga	agctgttgc'	300
cctgtgcaag	aagaatcaga	tctttgaaaa	aaaaaggaga	gaagctnaaa	gcatttgctt	360
caaagcatgg	ggctaacttc	agaaatcccc	ccattgggcc	ttcctnctaa	tncttncatn	420
ccttcaaaat	ctgtggagcc	ctttccaagg	tgaaacttgn	aannccaaga	antntggaaa	480
atggcncct	tggggaatct	agaccnaggg	nccttttttna	accttggaat	ngnttaaaaa	540
tcacnccaag	nttgactttt	ccttccttcg	anaaaaattgg	gtcccn		587

<210> 121

<211> 570

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(570)

<223> n = A,T,C or G

<400> 121

ggtagctctg	gtttatcaat	gggacgttcc	agcaatccac	acaagagctc	tttatcccca	60
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acatcactgt	gaataatagc	ggatcctata	tgtgccaaagc	ccataactca	gccactggcc	120
tcaataggac	cacagtcacg	atgatcacag	tctctggaag	tgtctcctgtc	ctctcagctg	180
tggccaccgt	cggcatcacg	attggagtgc	tggccagggg	ggctctgata	tagcagccct	240
ggtgtatttt	cgatatttca	ggaagactgg	cagattggac	cagaccctga	attcttctag	300
ctcctncaat	cccattttat	cccattggaac	cactaanaac	aaggctctgct	ctgcttctga	360
agncctatat	gctggagatg	gacaacttaa	tgaaanattt	aaanggggaa	aacccttaag	420
ccttgagggtg	tgtgnccact	tcanaggact	ttaaccttaa	ctttgagacc	aggccaacct	480
ggnaancctt	tgggtggagaa	attggccgaa	cttcccnact	ttggccagggn	ttttcccang	540
antgtcaaan	caagacttcc	ttatcatggn				570

<210> 122
 <211> 551
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(551)
 <223> n = A,T,C or G

<400> 122						
actatctcta	ttcaggatta	tgaagttttt	cgatgcgaag	attcactgga	tgaaagaaag	60
ataaaagggg	tcattgagct	caggaagagc	ttactgtctg	ccttgagaac	ttatgaacca	120
tatggatccc	tgggttcaaca	aatacgaatt	ctgctgctgg	gtccaattgg	agctgggaag	180
tccagctttt	tcaactcagt	gaggtctgtt	ttccaagggc	atgtaacgca	tcaggctttg	240
gtgggcacta	atacaactgg	gatatctgag	aagtatagga	catactctat	tagagacggg	300
aaagatggca	aatacctgcc	cgtttattct	gtgtgactca	ctggggctga	gtgagaaaga	360
aggcggnctg	tgcaggggatg	acataattcta	tatctttgac	ggtaaccatt	cgtgatagat	420
nccagtttaa	ttcccatgga	atcaaataca	attaaatcat	catgactacc	ttggttcccc	480
atcggttgaa	gggaacngnat	tcattggggg	ggcattggat	ttgatnnena	gnttttattca	540
atactttctc	n					551

<210> 123
 <211> 575
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(575)
 <223> n = A,T,C or G

<400> 123						
acttaataca	tattttcaaa	cctgtttgca	tttcaaacaa	agtttagcgtt	tttgtaaate	60
aaatttgata	acccgactaa	aaatattttc	cagcttttatt	atttaaggag	ctgcacagcc	120
tttaaagtgg	ggaccaggag	gcaggcagag	gcagagagac	tgaatgcacc	caggactgag	180
cagcagtcta	cagcaacatg	tcccacaact	ttgggtgctgg	aaacacaagt	aatgcacaag	240
acagctgccc	tccagtgtca	ggatcctgtg	aaacagcata	tcaaaagatc	gccagcttct	300
tataattttac	acacttttcat	ttaggattgc	ttttttgaag	aaaaatcttt	agaatgccca	360
tttttaattt	aatatccaga	accctggaat	ttaaaaaaac	ctaattngaaa	ggaaattaac	420
tggtaccatc	aaaaatgggg	ntgntgggtg	gancntgtgt	gaagttaggg	aattctatgg	480
cttttttttaa	gatgccccgg	aaaatttaac	cccttaatng	cangttttaat	ttngaattcn	540
cncaggtan	tgtatgtng	gctcanatta	gtanc			575

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actttctgct	ttangaggct	tgggggtgagg	ctgaanatct	gggggccaca	cttcgagagc	420
aaccaagact	gtaagtgggg	ccttccanag	cccaatgaag	ggaatactta	ggtacaggan	480
gtgtctgcat	ggncncangt	gtgggggttn	cttctcggcc	ttaaccagaa	agtatctctg	540
gttttaattt	taaaatgaaa	attttaaagg	gtgnctgaaa	cnaattgg		588

<210> 129
 <211> 588
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(588)
 <223> n = A,T,C or G

<400> 129						
ggtactgccc	tctccagatc	agcagttcag	gagagcacag	gaggcaaaac	acagattgct	60
gggcttattg	gtgccatcat	cgtgctgatg	gtcgttctag	ccattggatt	tctcctggcg	120
cctctacaaa	agtccgtcct	ggcagcttta	gcattgggaa	acttaaaggg	aatgctgatg	180
cagtttctg	aaataggcag	attgtggcga	aaggacaaat	atgattgttt	aatttggatc	240
atgaccttca	tcttcaccat	tgtcctggga	ctcgggttag	gcctggcagc	tagtgtggca	300
tttcaactgc	taaccatcgt	gttcaggacc	caatttccaa	aatgcagcac	gctgggctaat	360
attggaagaa	ccaacatcta	taagaataaa	aaagattatt	atgatatgta	tgagccagaa	420
ggagtgaaaa	ttttcagatg	tccatctcct	atctactttg	caaacattgg	tttctttagg	480
cggaacttat	cgatgctgnt	ggcttttagtc	ccttcgaatt	tacgcaagcg	cacaaacttt	540
gaggaaaatc	cgaaactgcn	aagcaagntt	gntacaagtg	acccaaan		588

<210> 130
 <211> 190
 <212> DNA
 <213> Homo sapiens

<400> 130						
ggtacaaaaa	aaaccttaca	taaattaaga	atgaatacat	ttacaggcgt	aaatgcaaac	60
cgcttccaat	tcaaagcaag	taacagccca	cggtgttctg	gccaaagaca	tcagctaaga	120
aaggaaactg	ggctctacgg	cttggaacttt	ccaaccctga	cagaccgcga	agaccccgcg	180
tacttttttt						190

<210> 131
 <211> 386
 <212> DNA
 <213> Homo sapiens

<400> 131						
ggtacagaac	tcagaggaaa	aaagaaatta	aatttttagct	ttctggagag	cagccctctt	60
ctggcaccat	caaacacttc	tttgtttccc	ttcaacttgg	aactcttcaa	acatcagggg	120
ttgtgaggg	ttggccattc	ttttatcttg	ggcccatgtg	agtgcagaaa	atgggtgcggc	180
ctgggaaaga	tctccctcct	ttacattttc	tcttctccct	cctcctcctt	attctaaaac	240
tgtgcctcca	acagaggggc	aggggctctt	gtagagagat	ccctggccca	ggacaggaga	300
tgccaaatct	aatttatctc	actgagggcc	tttgagaaaa	acgcttcagg	gccagggtca	360
gtggctcatg	cctatataat	cccagt				386

<210> 132

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<211> 593
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(593)
<223> n = A,T,C or G

<400> 132
actgagacaa tgggttagggg tgtttttctta attctttttcc tggtagggca acaagaacca 60
tttccaatct agaggaaagc tccccagcat tgcttgctcc tgggcaaaca ttgctcttga 120
gttaagtgc ctaattcccc tgggagacat acgcatcaac tgtggaggtc cgaggggatg 180
agaagggata cccaccacct ttcaaggggtc acaagctcac tctctgacaa gtcagaatag 240
ggacactgct tctatccctc caatggagag attctggcaa cctttgaaca gcccagagct 300
tgcaacctag cctcacccaa gaagactgga aagagacata tctctcagct ttttcaggag 360
gcgtgcctgg gaatccagga actttttgat gctaattaga aggcctggac taaaaatgtc 420
actatngggg gcactctaca gtttttgaaa tgctaggang cagaagggca aaaataaaaa 480
acatgacctg gttgaaggaa naaaagcaaa gaaacttggg ngggaggaca attaaaaaga 540
gnnctgaggga tccctnttc ttaggtccct ctcttacnaa ggacnctntt tat 593

<210> 133
<211> 588
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(588)
<223> n = A,T,C or G

<400> 133
acagancatt nnnagcnctn gcacaggnta cagaacctna cagacccaaa ggaacatcgg 60
ataggcnaag cgactacagg aggcgtgtgt gcgcttgggc naggtaaaca gggtcagtat 120
tggtcnngtg acaagagnca cgaantctgg ccngacantg angtnaanaa ggttnatntt 180
ttnacantta tnnnanatat nnnnnaannt attaanctgc ancanntgat ttnnacacct 240
anttactaga aaactaanga aagcactnat tagctctgaa tnaantnaca tggnaagcct 300
tttactaatc tncaanaaaa ccttctctgc antatnnnaa agattttatn atacaangng 360
gnnnatcnct cnatcatann gggttctatt ananaaccct gctaantntg cgacttacag 420
aacanccagc ntananatga ntttcatgcc catttgggaa gcatngcccg ggtatcacia 480
aggaaaccta ctaaagnttt ctgttatacc agccttctnt cntatcantg catgngnana 540
nanaacctt gaaggtntc cnggggactt tnttctnttn ctttgccc 588

<210> 134
<211> 618
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(618)
<223> n = A,T,C or G

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<210> 137
<211> 504
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(504)
<223> n = A,T,C or G

<400> 137
ttttncaaan nnaagttttt tacttccnaa aantna ggc taaggggngg gnggngggng 60
aaaaaagnaa aacaaaaaaa ccccaaaaaa atggggnggn naaaaggggg gganaaaaaa 120
ccnntntttt ntaaaantntn acaaggcaag ngcnnangga aaaaaaaaan ncctgnaaaaa 180
tccccncgg nnggggnaaa natnnnggtt tccttttgnt ttnaaacccn ntnangnaag 240
gntntcccc ntnccccctna atnaaaaatt tntntnccng ggccnnaacc nccntanggg 300
naaattccac cncnctgggg gccgttanta agggatccna gctnggccca ancttgngga 360
aacatggcaa aactgttcct nnggnaaaat gttccccctc anaattccca naaaataaaa 420
ccggaacata aagngaaaac cngggggcct aagngggncn cacnccattt attgggggtg 480
ccnccgnccc tttcaaangg aaac 504

<210> 138
<211> 386
<212> DNA
<213> Homo sapiens

<400> 138
acaacaaata acactgtgac tccaacctca caacctgtgc gaaagtctac ctttgatgca 60
gccagtttca ttggaggaat tgtcctgggc ttgggtgtgc aggtgtgaat tttctttctt 120
tataaattct gcaaatactaa agaacgaaat taccacactc tgtaaacaga cccattgaat 180
taataaggac tgggtgattca tttgtgtaac tcaactgaagc caaaatacta tcttttaaga 240
tgtcccatat ggaagacgct attccaggat ctttaaattt ccatggatgc atataggatg 300
tttgggagca tcatccgtga agaaaaaatc aattaaatca ttgtgttcaa caggaatatt 360
taaaataaaa aaaaaaaaaa agtacc 386

<210> 139
<211> 586
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(586)
<223> n = A,T,C or G

<400> 139
ggtactcaag tttataatgt ccccaaacct taagactaga aaatcatccc aagaaaaagg 60
cctatagtgt gtttaatttc accctgagaa tactgtgata aaaatcaata tatttcagag 120
ctagtaagta tttaaaaatt agtgtctcaa aaaggggaca tcataaggga aatacagggt 180
ttagagggtc gagctcaagt ggtgtaagac agttctttct tcttcctcct ttaaactctt 240
cactttgctc taacacggaa gatgggggac agtgatcccg aagggtattac taaaatattg 300
cagctttcag taattatgag aagcacagat atcaccagaa aagaaagcaa tcatttgagg 360

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tactaagaaa	cgaacaatg	ttatttggtg	gtgtataatt	ctacttttct	agtagattac	420
tgngtggaat	tctgtgaaaa	atatttgaga	aaangcctgt	attgcataaa	taaatctttg	480
tatgttgcaa	aaaaaaaaaa	aaaaaaaaag	acctgccggc	cgncccaang	gcgaattcca	540
cacctgccgc	cgtctagngg	tcaccccggt	ccacttgggt	atatgg		586

<210> 140
 <211> 591
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1) ... (591)
 <223> n = A,T,C or G

<400> 140	
acagggagga	atgtgaagta gatagaaacc gacctggatt actccggtct gaactcagat 60
cacgtaggac	tttaatcggt gaacaaacga acctttaata gcggctgcac catcgggatg 120
tccctgnacc	aaccttcaag gccnaaaccc nnntgggtgnn ttgggncnt aaatnaggat 180
ggccctgtnt	tcctagtgta acttgttccg ttgggtcaagt tattggatca attgagtata 240
gtagttcgct	ttgactgggt aagtcctnac cnngtccnt tngngtgggg tttttttagg 300
naaaagnctt	ttggtncatt nntggggggg gnaggggact gaacctttat tntttccaaa 360
tncaccttaa	antcaggggac aanaaacatt ccaanaacca caatctttta aaaaattaac 420
tngccagtgg	gaatgtttta aaanntnaan ggtctttttt gccttggttt ttgtgggggt 480
ctctcttccc	ccccctgggg ttaatttttn aagccgggac ctncnaana cccctttttt 540
caaagggcc	naaaccccc ccccnaaaa aaaaaaaaaa aaaaaaaanc n 591

<210> 141
 <211> 592
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1) ... (592)
 <223> n = A,T,C or G

<400> 141	
ggtacacaaa	ccaagacaat atcaggggtga cagggtgaatg aacttaaatt ctcagtcttg 60
tctattcacc	aaaaaagtat actgcctggt ttttctttaa ttattcaagg ttgatgactt 120
ttaggaaacat	gttttatact gtatttttta attaaagcaa gtgccttgat gtaattccat 180
gtaaatcatt	gcttaaccct cttatgggat gaggatgagt tattaatgta ttgcagccta 240
ctggaaagga	gggggagttg gttaatagca gatacttttc ttctagaagc ttatgtttta 300
tgctgtttat	tatgtaagat cctgtatgtg tggtgagatt tagaggtttc atttgttttg 360
tctgctaata	aattgttact ctaataataa ccnngnnaaa naaannnnnn nnnnnnnnnn 420
nnnannnggt	nctgcccng gcggccgctc gaaagggcga attccancca ctggcnggcg 480
gtactaaggg	gatccgnctc gggncccaac ttggcgtaat atnggcatac tggttcccgg 540
gngaaatggt	atnctgcaaa ttccccaaat acnaccggaa ncttaagggt aa 592

<210> 142
 <211> 595
 <212> DNA
 <213> Homo sapiens

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tctgattgng ttccttttaa tcttctctca tttctttttt attagactag atagtgattt 120
atctatttta ttaatttttt caaaaaatca cctcctanat ttgttgtttt ttaaggggtt 180
ttatgtctct atctccttca gtccaactct gatcttggtt atttcttgnc ttctgctaga 240
tttgggggtt gntttctgnt ggntctctaa gttctttttg ntgngacatt agattgncaa 300
cttaaaatct ttctagctat ttgacgtggg catttaatgc tataaatttc ctggtaacac 360
tgctttcgct gtatnccana naatctggga tgggtggggcc ttggtttcaa taanttcaa 420
tacctcttaa ggggngggag ccaanaagan ctaatagggg cagcactgct ctgggctncc 480
atcaanaagg acaaaaactg ggagngaccc tgcttnttca ctgaggnacc ggcccggccg 540
gccgtccnaa ggcgaaatcca cncnctggcg gccgtctatg gatccacccg gnccaactgg 600
ggaatatggc aaa 613

```

<210> 145
 <211> 345
 <212> DNA
 <213> Homo sapiens

```

<400> 145
acactgatct acaaaaatct taaaatgagc cggggcgcggt gactcacgcc tgtaatccca 60
gcactttggg aggccaaagc agggcgatca tgaggtcagg agatcaagac catcctgggt 120
aacacgggtga aaccccgctct ctactaaaaa taaaaaaaat tagccgggtg tgggtggcggg 180
cacctgtagt cccagctact cgggaggctg aggcaggaga atggcgtgaa gccgggaggt 240
ggagcttgca gtgagccgag atcacaccac tgcactccag cctgggcaac aaagcaagac 300
tctcaaaaaa gaaaaaaatt tttttttaaa tgagctgggt gtacc 345

```

<210> 146
 <211> 475
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1) ... (475)
 <223> n = A,T,C or G

```

<400> 146
actacaaggt ttagcatttg ctctgctggt cgacattccc ccagtctatg ggttgatatgc 60
atcctttttc ccagccataa tctacctttt cttcggcact tccagacaca tatccgtggg 120
tccgtttccg attctgagta tgatgggtgg actagcagtt tcaggagcag tttcaaaagc 180
agtcccagat cgcaatgcaa ctactttggg attgcctaac aactcgaata attcttcact 240
actggatgac gagaggggtga ggggtggcggc ggccggcatca gtcacagtgc tttctggaat 300
catccagttg gcttttggga ttctgcggat tggatttgta gtgatatacc tgtctgagtt 360
cctcatcagt ggcttcaact ctgctgctgc tgnatgttt tggtttccca actcaaattc 420
atttttcaat tgacagtccc gtcacacact gatccagttt caattttaaa agacc 475

```

<210> 147
 <211> 629
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1) ... (629)
 <223> n = A,T,C or G


```

<400> 147
cgagggtacgc gggatttgaa tcttaaactg tattttttctc ttagtattgc taatgagtaa      60
agaaaagtct cataaggtag ccaaataaaa aagaatgaaa gggaaagtga aaaattaagg      120
ggacaaaaga tgggatgtga aaagaagaat tctagtttga tggtgactca tattcacgat      180
aggatacaaa gtgtgatttg ttggaaacat gtcccaaatt tctaaaattc tgcttctctg      240
ccaaaagcaa tgtctttctt ggttgatatt tgagttttta aagggtcaaa tctttctaat      300
tttttgatc tttagagggc agcactagaa gaaatcagca ggtctaacc caccagtaag      360
aaaactacca cttcttgatt ttacagatt taaaaaaatc ttttcagtgc ctttctttt      420
aatgtaata caaatttaaa cctangctta atatagcgtt tccctttccc caagtgatgt      480
cnaggtcgat gccaaatcaa tgatccnaaa tgatcgnggt naaaataact caaagggttc      540
ttaagngag tngcatgcca aaaaatacct tgattccggg ggtttggacc tggctttgtt      600
ggggcctntg aaatgccaan ttanccan
629

```

```

<210> 148
<211> 614
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(614)
<223> n = A,T,C or G

```

```

<400> 148
acaaaagagc ctgattcttt ttaattccac aaatacctag catctcaaag taacatgtaa      60
acaaacttct atgctgtctc atgaatcctt ccaatttcga taataaacta aatagtattg      120
gatctagtat atgactttca tgtgtaagtt atggttctat ccattacttt aacaatatta      180
ctgatgtaac agagaaaaat tttcaactat tgtattttatt taaaacaaac tgacaagttc      240
aagcacctgt cttcagaaaa gccagcagca tttttttttt ttaacatact caaagtaaga      300
tttggcctaa gcccttaata cttttctgaa cagccatgca actaaacacc ctcagggaga      360
tgttacataa gggagagaag aacatggagc aatttgcact ttttccctag ataataattaa      420
caaggnaaag caaatncaga tctttatgaa tgaatggntg gcatggttta tcacttggac      480
tttttaact agagncncta tcatattggt aaatagaaan aaaggatttt aataaagctc      540
tncctgcttc aaaattaagg ggacnttttc tgggaggcct tcagggacca taataaggta      600
aaaggggacg gttg
614

```

```

<210> 149
<211> 628
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(628)
<223> n = A,T,C or G

```

```

<400> 149
nccgaggnac tttntttttt tttttttttt ttttnaacag cgncttttca tttttattac      60
tcaaaaaagt ttcatttttt tatttaagct ttctgactct gngcttgggc cttcaacact      120
ttcacaacga ttttctgtct ctcgataagg aaagcccgct tgatcctana aaggaaaata      180
ccaaattaat catttcttta aaatgaactt cattttttat ttagcccaaa aaaggnaaac      240
atggtaaaga accaagcnaa gcaatcaggg aaccaggaa actacnggat acccaaatac      300

```

ngagtaaaac	ttaaaaagggg	aaattcattt	aaagcagggg	aatccctcaa	tttcatgccn	360
gtagttatct	gncctcctct	gagcaagaat	aactatgaag	catccccag	gagaccacnt	420
atgagactta	attattggta	ggatccagga	atagnngnat	ttnttgattt	gcaaaangtn	480
taaaaaattt	taaccctntt	ttgaaaattc	ccagnaaaa	caccncataa	ggggctntgt	540
gttaaaacta	aaattaaagg	gaagggtttt	tccagaaacc	cccccanac	cagggtttna	600
accggttang	gcanntcncc	aaaccnan				628

<210> 150
 <211> 509
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(509)
 <223> n = A,T,C or G

<400> 150						
ttgggggaann	aaaaaaaaaac	tttttttttt	nggggnnnngg	ggntgcnanc	natncaaaaa	60
tcaaaaancnt	ntttgggttt	taactttttt	ttttttgntt	gncaaannaa	aantaaantt	120
tnntttttana	tttgctaang	ggccngancn	gcnnaaaaaa	nccttttttn	ggggaanctr	180
nggggcaaat	tnnttnancn	accctttggg	anaacttttn	ttaggggggn	nnnaaccgnc	240
atttttgccc	acttttttcc	cttttgntta	anggggncc	tgggcnggac	cnccttagg	300
ggnaattcac	ccnctggggg	gcgttatntt	ggatccactc	ggnccaactt	gggggaaaaa	360
gggaaaacnt	tttctggggg	aaattttttc	ccncnaaatt	cccaanaana	aaaccggaac	420
nnaaanttaa	accggggggc	ccaaggnggg	ccnncccntt	nttgggtggg	ccctgccent	480
ttaangggaa	attttgccc	tttttaaaa				509

<210> 151
 <211> 622
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(622)
 <223> n = A,T,C or G

<400> 151						
ggtacttttt	tttttttttt	ttttttttgc	tttggacaaa	tttattgaaa	catacaggcg	60
gctggttagca	gagaaatcat	tccatgattg	atgtgttaca	tttggccact	accttgaatg	120
tataatttaa	aaatttatatt	tttcacaact	aagccttttg	ccaaaaaagt	catttagcac	180
atctttaaag	atcaataaga	aatggatttt	ggacattaaa	aagatcaagt	cactgaatta	240
aacagtagca	acccccatta	atctagaatc	ccatagtgtc	gaaggtagag	gtgtctgtgc	300
aaagctagtc	atttgttaac	agcaatcana	aaanatgggg	gcaggcacac	ctgtcaaaag	360
tggcaacana	netggcagga	caggacggct	gggctgggtc	ggtcaggtga	gcatgtacca	420
aaaacagcag	caacagaaaa	cccgtccacc	angcttgtga	agcangtgga	tggtcctagc	480
tcattctntn	ttttggnctt	ntancacata	cactgngggg	ttangangnt	tctgaggnc	540
accttgccnc	cctacctgcc	cgggngggcg	ttnaaagggg	aattccacca	ctggggggccg	600
tctaattggga	cccacctggg	cc				622

<210> 152
 <211> 313

<212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(313)
 <223> n = A,T,C or G

<400> 152
 acggtggatt agttcttttc agcatgttcc ttctgtatga taccagaaa gtaatcaagc 60
 gtgcagaagt atcaccaatg tatggagtcc aaaaatatga tccattaac tcgatgtga 120
 gtatctacat ggatacatta aatatattta tgcgagtgc aactatgctg gcaactggag 180
 gcaacagaaa gaaatgaagt gactcagctt ctggcttctc tgctacatca aatatcttgt 240
 ttaatggggc aatatgcat taaatagttt gtacgcgggg aaaaaaaaaa aaaaaaaaaa 300
 aaaaaaaagt acc 313

<210> 153
 <211> 620
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(620)
 <223> n = A,T,C or G

<400> 153
 cgaggtacgc gggagggcaa caagaaccat ttccaatcta gaggaaagct cccagcatt 60
 gcttgctcct gggcaaacat tgctcttgag ttaagtgacc taattcccct gggagacata 120
 cgcacaaact gtggaggtcc gaggggatga gaagggatgc ccaccacctt tcaagggtca 180
 caagctcact ctctgacaag tcagaatagg gacactgctt ctatccctcc aatggagaga 240
 ttctggcaac ctttgaacag cccagagctt gcaaccctagc ctacccaag aagactggaa 300
 agagacatat ctctcagctt tttcaggagg cgtgcctggg aatccaggaa ctttttgatg 360
 ctaattagaa ggcttgact aaaaatgtcc actatggggg gcactctaca gtttttgaaa 420
 tgctaggagg caaaaggggc agagagtaaa aaacatgacc tggtagaagg aanaaagcaa 480
 aggaaactgg tggggaggat caattagaga ngaggccctg ggatccnct nttcntaggn 540
 ccctctcata cnaaggacac tttttatatg ccttcccaaa ctgntnggga agggtnaaac 600
 caaaatccgg ggtanaacct 620

<210> 154
 <211> 339
 <212> DNA
 <213> Homo sapiens

<400> 154
 ggtacctgga ggatatagac ctgaaaacac tggagaagga accaaggact ttcaaagcaa 60
 aggagctatg ggaaaaaaat ggagctgtga ttatggcctg gcggaggcca ggctgtttcc 120
 tctgtcgaga ggaagctgcg gatctgtcct ccctgaaaag catgttggac cagctgggccc 180
 gtccccctct atgcagtggg aaaggagcac atcaggactg aagtgaagga tttccagcct 240
 tattttcaaag gagaaatctt ctggatgaaa agaaaaagtt ctatggtcca caaaggcgga 300
 agatgatgtt tatgggattt atccgtctgg gagtgtggt 339

<210> 155

<211> 450
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(450)
 <223> n = A,T,C or G

<400> 155
 cgaggtactt tttttttttt tttttttttt tttttcttat ttttgtttaa tttatttaan 60
 accacctnct tacaacttnc anagagaaaa tacaaaacaa gaaacanact tggtttnaaa 120
 tgcataacca gntgctggan tttaaagcat tactgataac attgtttacan aanaatggca 180
 nnttactcna gggcacttna gtattcctna ggaataaaca ttgatttctc ttgtcctccc 240
 nntgggatgt tctcangtna agtcactgcn cctgcnctta gacatatttt ccatgtnnca 300
 naananggag cctgnaaant atgctnacag tnggaataag ccattnctaa ttccatgcca 360
 naaccnangg ctaatggnc attctttttt aataaggtat gtggaaaana ttcntatccc 420
 aaanaaaant tgcccggncg gtctntntaa 450

<210> 156
 <211> 760
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(760)
 <223> n = A,T,C or G

<400> 156
 cgaggtactg cccagtgaa aatggaactg aaagagcctg tagctgtcag agaaaggacc 60
 acctttcagc actgatcggt tatcgttgtc ctcaaaattt acatggaagg aatgccccac 120
 attgataatt tctttggctg tggctgggtt gtaggagaca ctaatagggt tcagagaggt 180
 gtcattgttt gtttactggt tttaatatc aacaggggac tggttatttc cattggcaat 240
 gggatacagc ttgtctccatt gttcaggacc atttttgtca tcatatcccc agtctggact 300
 tgccattatc ttctactgag ttttcttttt ctgaaaacaa aaataatacc tggataaact 360
 aactgcccc gcgtcctgcc cgggcggcca aaggggcaat tccaccactg gcggccgtac 420
 ttatggatcc aactcgtccc ancttggcgt aatatggcat aactgttctg nggnaaatgt 480
 atcccttaca attcccnac atcnaccga acctaantgt aancctnggn gcnnataagg 540
 actactnctt aatgggtggc tctgcncttt caannngaac cttngcnctn gntatgattg 600
 ccaccccgga naggggtggt ttggccttcc ntcttgtaann aatcttcncg gnttggttga 660
 anggtnttct taggggatng ttccaatggg gaccgnaanc ttccagccna ggcaccaaen 720
 cnttggttta nccccacnn aaaantanag gggcnggggt 760

<210> 157
 <211> 668
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(668)
 <223> n = A,T,C or G

```

<400> 157
ggtacccagt agtcattcag gaacagggtt ttcagtttcc atgtagttga gcggttttga      60
gtgagtttct taaacctgag ttgtcgtttg attgcactgt ggtctgagag acagtttgtt      120
ataatttctg ttctttttaca ttgtctgagg agtgctttac ttccacctat gtggtcaatt      180
ttggaataag tgagatgtgg tgctaaaaag aatatatatt ctgttgattt gaggtggaga      240
gttctgtaga tgtctattag gtctgcttgg tgcanagctg agtcaattcc tggatatcct      300
tggtaacttt ctgcttggtg ntctgtctaa tattgacagt ggggcgttaa agtctcccat      360
attattgtgt gggagtctaa tctctttgta ggtctctaag gacttgcttt ataaactggg      420
tgctcttgat tgggtgcaat atatttagga tagttagctc ttcttggtga atggancctt      480
taccaatatg aatggcctcc ttcttttga ccttggtggg taaagctggt tatngaaact      540
ggatggancc ctgctttttt tgggttcattt cttgnagggt cctcagcctt attttancnn      600
gnggctttgn ccncntccg cggcnttaag ggaaccacnc tgn gcgtcta ngancactgg      660
caactggg
668

```

```

<210> 158
<211> 737
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(737)
<223> n = A,T,C or G

```

```

<400> 158
tttttttaag ggtcaatggt tacatttttt tcatataaat atcaagttgt cagcaccatc      60
tgttgaaaaa aatcttttga atggctaata ttttatgtca tttagatttga taatagttta      120
agaatttttg ttcctatatt catgagggtt gctttccttt aacttttttg ttttgtaatg      180
tctgtgtcag gntttactat tagaacaata ctagtctagt aaaaaaaaaa anaaacaaaa      240
aactancaag tgtntctccc cttctattta taanaanggn gttacttctt ccttaaattg      300
nnaaattatg agngaaaact ggagtatcnt tgcnggantg gaagtttcct tgtggaaaga      360
attttatnat nattacattt caatagtncc gctccctgc ncgggcgggn ntcaaaggcg      420
aatncagcaa attgntggcc gntactnngg accaactcgc gncatnntg ggnnancang      480
tcaanctgtt ctngnnaatt gtnccttcc aatncccaca nanaaccgaa cctaaatgga      540
accnnggggc tantaangnc tacnntatt gngnggctnn gccctnnnt ggaaactgnt      600
cnacnttat aatggccccc cnggaaggnt tntttggcct tctnntncaa anctggcngg      660
nttntgtgna ggttatctna ntggatgttc cacgggaacn gaanatntan ncagtggacn      720
aaanntnntn ttttntct
737

```

```

<210> 159
<211> 739
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(739)
<223> n = A,T,C or G

```

```

<400> 159
cgaggggtaca ctgtgagaga ataacatgga cttgatatgg catcacactt gttttaaagc      60
aaaaaaaaag aaaaaaagaa aaaaaagaaa gtacagttaa aaagtaagca ttgtagtaaa      120

```

tagtggattc	tctggtgtgt	atTTTTtAtc	tCagtgttga	aaattggaaa	agaatgggct	180
gaagtctaaa	aactggaata	atgaaggaca	ctaaatgcct	ttattgtaga	tactatgttt	240
gtaagtctat	agctaagcaa	cttaagccaa	aaaggTcttt	caactgaagc	tttaatcaac	300
ttatTTtgga	gatgttctct	tccttatctc	atgcgtcatc	cctaaaataa	taagatacat	360
gggatcaaat	aacccttgcc	TTTTcaacac	aaatcagttg	gaaaattatg	ggttgagtcc	420
tgttgctgcc	atggttctgt	tctcaaaatg	agtgtgtatg	acatcccatc	tatgtaatag	480
gctacctttt	tggctcttgg	aactttgtcc	tgcgcggccg	ccnttaaggc	nantcnacca	540
ctggcggcgg	tactatgggn	tccagctcgt	ccaaccttgc	tatcntggct	acttttctgg	600
ngaattgtatc	cgtncatccc	cacttcancg	gagctaangg	aancntgggc	ctatggggct	660
actccatattg	ctngccnctg	cnttcnangg	aacncgcntc	ttaanatgca	cccnggaagg	720
gtngtngcct	tctttcttt					739

<210> 160

<211> 802

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(802)

<223> n = A,T,C or G

<400> 160

cgaggtagag	cagagacctt	cctgcttttt	actgggggact	ccagattttc	cccaaacttg	60
cttctgttga	gattttttccc	tcaccttgcc	tctcaggcac	aataaatata	gttataccac	120
taaaaaaaaa	aaaaaaaaag	tacgcggggg	cccatgtgtt	ttgtaatctc	tgaggagaag	180
cagcagcaaa	catttgctag	tcagacaagt	gacagggaat	ggattccaaa	caccagtgtg	240
taaagctaaa	tgatggccac	ttcatgcctg	tattgggatt	tggcacctat	gcacctccag	300
aggttccgag	aagtaaagct	ttggagggtca	caaaattagc	aatagaagct	gggttccgcc	360
atatagattc	tgctcattta	tncaatatga	ggagcaggtt	gactggccat	ncgaagcaag	420
aatgcagatg	gcagtgtgaa	gaaagaaaca	tatttacctt	taaagcttgg	tcccttttna	480
tcgacchaag	tggccgaca	agcttggaag	attactngan	aaagctcaat	nggactatgt	540
gactcttttt	aataatttcc	anggnTTtaa	acccgtgagg	acttttcccc	cgntaaatgg	600
aaagtatttt	gcnannggac	ttgacttccc	ggngccntaa	gngaattcac	cactgggggg	660
gnTTagggtc	cnnttggnca	anttggnaaa	ngggtaatnn	cntgnaatgt	tccatcatccc	720
aantngccgn	ataantaacc	gggcaaaagg	cccaaattgn	gccctccttn	nngaattnanc	780
cctntannna	ancggggggg	gg				802

<210> 161

<211> 214

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(214)

<223> n = A,T,C or G

<400> 161

acttttnntt	tattcnttat	ttttgggacc	tgtctctact	gtccaccag	actggagtgc	60
antggcacca	ttatagctna	ctgcagcctt	gacctnntgg	gtcCaagtga	tctnctgtc	120
tacaccccc	aagnatgntg	tgacattatg	cttgataat	acttgtatnt	tangtaaaga	180
cagggtcttt	ccnatnnacc	nggnagatct	naaa			214

<210> 162
 <211> 304
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(304)
 <223> n = A,T,C or G

<400> 162
 acttaggaat acaactatat acatatgatt ttatTTTTTaa gaccatatta tatttgggta 60
 tctactaata ttttGTataa agcaatTTTT tgt catta cgtgactttt tgTTTTattg 120
 tatatgtaat ttaacacaca ataaagggtta aagttgcttc cccaaaccac actTTtaatc 180
 aaaacctaga atcatctgca gtccttgTTa aaaatgcagg tttctagaac cctctgaagt 240
 tctgattaaa taaatttatt gcaaatacaa naaaanaaaa aaaaaaaaaa agnccccggg 300
 gnta 304

<210> 163
 <211> 461
 <212> DNA
 <213> Homo sapiens

<400> 163
 actagagcca gtcacCctta acaaatcttt tcacattTTta tttctttcac atgtagtcac 60
 cttcaaaaaag gaaagatttg gaattTTtaga aaaggggcaa ctcttctttt tagcattctc 120
 atcagaaaagt cacaaaaatc gatggaatca tttccactgg gaagattgac cttttgtatt 180
 tatttGTggg gtaaattaat aagcattcca gatgcttgca gcttcctgca tccaggagat 240
 gctgtgttcc ccgtgatgca gctggaaccc aagctgcagc aggagatgca agtttcagga 300
 tgttccccac tgagctggag gaatatctac agcagtgatg cttgaaattt tgtatgaatt 360
 attttGTcgc ctaccctttt cctccaaaca aaaattagag gattattTaa tccttgggat 420
 cttccctttt ttgagaaata aagtttttat caaaaaaaaa a 461

<210> 164
 <211> 345
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(345)
 <223> n = A,T,C or G

<400> 164
 tttttttgag acaaggTctt actctgtcac ccaggctgga gtgcagtggc atgatcttgg 60
 ctactgcac cctctgcac ccaggTtcaa gtgattctcc tgtctcagcc tcccttgtag 120
 ctgggattac agccacttgC cactgcaacc ggctaatttt tgtattctta gtagagatgg 180
 ggttttacca tgttggccag gctggTcttg aactcctgac ctcaagtgat ccacctgcct 240
 ccattgtccaa agtgctggga ttacaggcat gagccaccac ccctggccta agtcattaat 300
 ttaaaaaatg ttattaggat gancgacctg ccgggCggcc gntaa 345

<210> 165

<211> 385
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(385)
 <223> n = A,T,C or G

<400> 165
 actgaaacag aaactntacc caattgcagt ccatatgttt tctgggatcc cggagttccc 60
 tttcaacaat gtaaaatata nacttaggtc aaaagttccc atgtctgaga aaactcaagc 120
 caaatcagtt ctctccaaa gttgacagga tttatgcttt aaaaatagag atacagaatt 180
 ctctttggaa agatctacca aattcctgta agaaaca .c taccctaaagt aggggaaagg 240
 ctatatgana agttcaaggc acttcttaaa aatatactt aggttttagg gaaaggaaac 300
 agacaagttt ccagaccgt ggggtggaatg gatgtagcag atcactgaga gggtacaagc 360
 gccgacctng gccngacac gctan 385

<210> 166
 <211> 745
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(745)
 <223> n = A,T,C or G

<400> 166
 tttttgacga tgtctctcaa caatacctga agtttctcat actcatcatc ccaagtctga 60
 aaaacttcaa agcatgctac cataactttt tcaaattctt cataagcaac atgcatcaat 120
 ttcttagtgc ccaatacttt gagtaattga gaactcaagt ctcttgaaat tgcctccacc 180
 aaacgcagtg ccctctgaat aggatatttt gtgtttcgga tctttctcaa atcccgcgta 240
 ctttgagaag ctgaggcggc agatcacttg aggccaggag ttcgagacca gtctcgtcaa 300
 catggcgaaa ccctgctcta caaaaaaaaaa aaaaanaanaa aaattagcca gacatggngg 360
 cccacatctg tagtcccagc tacttganan gctgaggcat gagaatagct tgacctggaa 420
 nggcaaagggt ttantgancc caaactgncc ctggattcca atnnggngga cccagtgana 480
 tttgtctcaa aaaaangaaa ggaaaaaaga gcccngcgga aggaaggatg gattgangga 540
 aaattgtggc ctccnnnnaa aggnccaang gccctnangt ttctttgaat agtttcctn 600
 gccnttctta ngggcctnng cctttttttn nnctggcgaa cctaggnatt cacatggggg 660
 ttangacncc gccnctggga naggaaagtn ctggaagnnc ncntcccaat ancgmntang 720
 aacgggcngn ggannaatttt tttnc 745

<210> 167
 <211> 623
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(623)
 <223> n = A,T,C or G


```

<400> 167
accagccact gcaaaaacat gccaaattgt aaagaccatc gaggctggga agaaactgca      60
tcaactaacg agcaaaaataa ccagctaaca tcataatgac aggatcaaat tcacacgtaa      120
cactattaac ctgaaatgta aatggactaa attctccaat taaaagacac agactggcaa      180
attggataaa gagtcaagac ccatacagtgt gctgtattca ggagacccat ctcatgtgca      240
gagacataca taggctcaaa ataaaggaat ggaggaagat ctaccaagca aatggaaaac      300
aaaaaaaggc aagggttgca atcctagtct ctgataaaac agatttttaa ccacaaagat      360
caaaagagac aaagaaggcc attacataat ggtaaaggga tcaattcaca agaagggcta      420
ctattctaaa tatatatgca cccaatacag gacccccaga ttcatagaagc aaatccttga      480
gattnccaaa ggattaaact cncncngtat tatggagact tncaccact ntnacctttc      540
ccgatcttgn cccaaagtac cnggtttccc gaattgactn gtttgncann gggctattaa      600
tttngaattt cncccaaaaa aaa                                     623

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```

<210> 168
<211> 703
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(703)
<223> n = A,T,C or G

```

```

<400> 168
ggtactccct gtttgctgca gaatgtcaga tattttggat gttgcataag agtcctatct      60
gccccagtta attcaacttt tgtctgcctg ttttgaggac tggctggctc tgtagaact      120
ctgtccaaaa agtgcattga atataacttg taaagcttcc cacaattgac aatatatatg      180
catgtgttta aaccaaattc agaaagctta aacaatagag ctgcataata gtatttatta      240
aagaatcaca actgtaaaca tgagaataac ttaaggattc tagtttagtt ttttgtaatt      300
gcaaattata tttttgctgc tgatatatta gaataatttt taaatgtcat cttgaaatag      360
aaatatgtat tttaagcact cacgcaaagg taaatgagca cgttttaaat gtgtgtgtgc      420
taattttttc cataagaatt gtaaacattg actgaacaaa tacctatatg gattggtaat      480
gacttatgag caantgctt ggccagacag ttacccaaac tttatatatn tnngaaggta      540
tacactngta aatctctggc taancgaatg cntccagggg taanngggtn tggntggant      600
aaanaatgcc ctgcaaaaaa aaaaaaaaaa aagccttccg nggccttnaa nggaatcnnn      660
angggntnnn ggccactggc cactggnaaa ngnaacgtct gga                                     703

```

```

<210> 169
<211> 609
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(609)
<223> n = A,T,C or G

```

```

<400> 169
acgtccatct tccagctgct tgccagcaaa gatcagtctc tgctgatcag gaggaattcc      60
ttccttatcc tggatcttgg cctttacatt ttctatcgta tccgagggtt caacctcgag      120
ggtgatggtc ttaccagtca gggctcttcac gaagatttgc atcccacctc tgagacggag      180
caccaggtgc aggggtggact ctttctggat gttgtagtca gacaggggtc gtccatcttc      240
cagctgtttc ccagcaaaga tcaacctctg ctggtcagga gggatgcctt ccttgtcttg      300

```

```

gatctttgccc ttgacattct caatgggtgtc actcggtctcc acttcgagag tgatgggtctt 360
accaagtcag ggtctttcacg aagatctgca tcccacctct aagacggagc accaggtgca 420
gggtggactc tttctggatg ttgtaatcag acanggtgcg ttcattcttc actgnttcca 480
caaaaaaaca cctctgctgg canganggat ccttccttnc ttggactttg cctgacattc 540
tnatgngnta ctccgctccc ttcaaagggg tgncttacan tcanggnctt acnaaaattt 600
cntccnctt 609

```

```

<210> 170
<211> 617
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(617)
<223> n = A,T,C or G

```

```

<400> 170
acaaagaaca tgtagctata ggaaataata gtgtaaataag cagtataata actggcccat 60
gtaaaataca aaaatattca ctgaagtcag gttttctata aaacagtgtt tattagaggt 120
atctttactat gaatcaggca tataatctga atgtagaaac ttttagaaat attaacagca 180
ttcagtcagt gccatgcact tgtgcttcca attatttttt taaagctgct ttgttttgac 240
tcatgtgaaa tagttaaggc ctacattctt atacacatta tccattctac aagggttaaca 300
atctttacact aaaacacagt ttaaattaaa aacgattttg aaaaattaca tctatattta 360
atccctaaga agtggttttaa gctggtaatg cagctcgctg tagctctaag agaggggtta 420
gtcaggaatc tgatcttgag ccataaangg tttcaggcta aacaaagaac aaatttaagt 480
gacagaaaat attataattn caatatactc agtttttttg tataaaatac cctgctagca 540
tgccactggc tatattgngg gcataatata aaatgncggg ggggggggat gancctccaa 600
gncaaanntt ggaccca 617

```

```

<210> 171
<211> 621
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(621)
<223> n = A,T,C or G

```

```

<400> 171
acagtatggg ggttgtaaat tggcatggaa atttaaagca ggttcttggt ggtgcacagc 60
acaaattagt tatatatggg gatggtagtt ttttcatctt cagttgtctc tgatgcagct 120
tatacgaaat aattggtctt ctgttaactg aataccactc tgtaattgca aaaaaaaaaa 180
aagttgcagc tgttttgttg acattctgaa tgcttctaag taaatacaat tttttttatt 240
agtattgttg tctttttcat aggtctgaaa tttttcttct tgaggggaag ctagtctttt 300
gcttttgccc attttgaatc acatgaatta ttacagtgtt tatcctttca tatagttagc 360
taataaaaag cttttgtcta cacaccctgc atatcataat ggggggtaaag ttaagttgag 420
atagttttca tccataactg aacatccaaa atcttgatca gttaaaaaat ttcacataac 480
ccacttacat ttaccaactg gaagaataat caatctctca agcatgggat tattagaatc 540
aacantttga aagctgtcct tgaaggctaa taaaaaagnt tgtctaacct ttcatgaggn 600
cttntnttta ctnccttaacn g 621

```

<210> 172
 <211> 399
 <212> DNA
 <213> Homo sapiens

<400> 172
 actcaaaatt acacatttgt ttaaataaat atccacacaa attctcagtt acatcaagta 60
 gctggtttat atttagatta tctcaagtag gggggaataa ccatgtgtag gaattcatag 120
 aaaaataaac aatcagctga agaggtctaa gaaaatgctg acttttaaaa ttccacttat 180
 ttcccttgaa gttttctacc ctcccatcg atgataaacc aagatcatgt aatggaaaat 240
 ttcaaccag ggctaaattc taaagtaaag cttcaattca agcccttccc ccaagagaat 300
 taattttcct gattttctct tctctcacat ctaaggagaa catttttaggc agttaaat 360
 cagaacttca aggtttcatc agggtcacct ttatgtacc 399

<210> 173
 <211> 616
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(616)
 <223> n = A,T,C or G

<400> 173
 actttgtgga taagaaaatg gaggaacaca tctgatggag agtgggcatt tgacaacaat 60
 ggaacaggta acctgcatgt aaaatcaaaa tataagtgtc tttttaagag ctgaaagctg 120
 ctgctggtca ttcattaatg tgctcagacat ttaatcagga tgctggacct tcaaaataac 180
 tgaaaaaaga accaagaaaa ggcgtttttg ttttcaacaa actttactaa ataaccctgg 240
 aaaggcaatg aacgatctga caatttaagc tctaagtatt taaagctcag ctagaagaaa 300
 gtgaggcatg acatatactg tcaacggagg gtgaaggagg canatttctg gaaatgcaat 360
 gatccccacca ttgtcttcaa ngagaaacct gcanacatat ttccangtct tgntaagt 420
 caactgtnta tttgtaatca atcatttngg aaaagtctgc tatgtaactt angncactgt 480
 gccccnacc accgatgaaa aggaaaaacc cctgacacca ggaaaatcct tccatcctca 540
 aanaaattaa gngaccaacn tttaaagaaa aaaaatnanc ccncctctnt ttacaaatnt 600
 ttcttccaaa tnttcn 616

<210> 174
 <211> 631
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(631)
 <223> n = A,T,C or G

<400> 174
 ggtacgcggg gacacgcacg ccgggcgtgc cagtttataa agggagagag caagcagcga 60
 gtcttgaagc tctgtttggt gctttggatc catttccatc ggtccttaca gccgctcgtc 120
 agactccagc agccaagatg gtgaagcaga tcgagagcaa gactgctttt caggaagcct 180
 tggacgtgc aggtgataaa cttgtagtag ttgacttctc agccacgtgg tgtgggcctt 240
 gcaaaatgat caagcctttc ttccattccc tctctgaaaa gtattccaac gtgatattcc 300

```

ttgaagtaga tgtggatgac tgtcaggatg ttgcttcaaa agtgtgaagt caaatgcatg      360
ccaacattcc agttttttaa gaaagggaca aaagggtgggt gaattttctg gagccaataa      420
ggaaaagctt gaagccacca ttaatgaatt aatctaataca tgttttctga aaacataacc      480
accattggct attttaaact tgtaattttt ttaattttcc aaaatttaaa ttggaanact      540
taaccccant tgccatntgn gtgacaataa aacattatgc taccntttt aaaaaaaaaa      600
aaaaaaaaaa agtcctgccc ggcggccctc a                                     631

```

<210> 175

<211> 261

<212> DNA

<213> Homo sapiens

<400> 175

```

acgaacctac agttttaact gtggatattg ttacgtagcc taaggctcct gttttgcaca      60
gccaaattta aaactgttgg aatggatttt tctttaactg ccgtaattta actttctggg      120
ttgcctttgt ttttggcgtg gctgacttac atcatgtgtt ggggaagggc ctgccagtt      180
gcactcaggt gacatcctcc agatagtgtg gctgaggagg cacctacact cacctgcact      240
aacagagtgg ccgtcctaac c                                     261

```

<210> 176

<211> 616

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(616)

<223> n = A,T,C or G

<400> 176

```

cgaggtagtc tgcttttttag gagatgaggt aagacatata catagatggc ttttactagc      60
caaggcaatg taaatggact aagattctca tgtgacttga ggttatctga tgaatttatt      120
ctcttcaaaa ccacctacct ttagagggca tgtttaaccc ctctctttat ttaaggaggg      180
agagaaaaac acatgtaacc agaattcaga gtgggttact caacctaaga gaacatacgg      240
agttctcttt gggaaaacaa caagactaca gtgttcactt cgcaccatga agtggcactc      300
ctgttatggc tgtcagagtc ctctcacttc ttatgaaagg atgcatctga ttctgaaatt      360
actgatatat tcatcagtt anggatgttt taaaaagtga aaacaaatgc cacacatata      420
ctttctagct ttcttgaaat caccgcacac attccaaaaa tagagaattc cctattactt      480
ttagagaaat ttccatatan tcttggtnaa gaancagtt gngcntattc caatttcagg      540
gtcttggttt ttgcccnaac ccaagtgttt cntntttta nggcttttca tggccgattt      600
naaaccttnt ttgtgg                                     616

```

<210> 177

<211> 632

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(632)

<223> n = A,T,C or G

<400> 177

```

cgaggtacag gtcagagtct tcttttcttt tctttttgag atggagtctt gctctgttgc      60
cagactggag tgcagtgggt cgatctgggc tcactgcaat ctccacctcc cgggttcaag      120
cgattctcct gcctcagcct cccgagtaac tgggactaca ggtgtgcgcc accaagccca      180
gctcattttt gtatttttag tanagatggg gtttcacggt gttggctagg atggtctcga      240
tctctggtca gaagtctttt ctgtaaatat ccttggtaaa gaagcaattt tagactgtag      300
ctggttgcaa tgctttaagg aagaagcaaa acaactgtca gtcttctga aatgaaaaaa      360
ctacaccagg gctgctatat caaagcaacc ccaaccagca cttcaatcat gatgccaca      420
gtggccccac tgagaaacca agaaaagttn cagatacaaa actgngatgc tcttgctatg      480
gnaatattgc nggcngtanc caagttagaa accaaacaag cntanggcc cgttnttttt      540
tgycggtgatt ttggcaanaa aaaaaactgg gngngtgggt ngggttccca ttgtaccccc      600
aaaaaacttn gggatgggtt aaagcccnng gc                                632

```

<210> 178

<211> 611

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(611)

<223> n = A,T,C or G

<400> 178

```

actttntttt tttttttttt tttttttttt ggatttagtt tttatttcat aatcataaac      60
ttaactctgc aatccagcta ggcattggag ggaacaagga aaacatggaa cccaaaggga      120
actgcagcga gagcaciaaag attctaggat actgcgagca aatgggggtg aggggtgctc      180
tcctgagcta canaagggaat gatctgggtg ttaagataaa aaacaagtca aacttattcg      240
agttgtccac agtcagcaat ggtgatcttc ttgctggtct tgccattcct ggacccaaag      300
cgctccatgg cctccacaat attcatgcct tctttcactt tgccaaacac cacatgcttg      360
ccatccaacc actcaatctt ggcagtgcag atgaaaaact ggggaaccatt tgtgttgggt      420
ccaacatttg ccatgggaca aatccangac ccgtatgctt taagatgaaa ttctcatctc      480
aaatttcttc ccataaatgg acttgcenca tgccatnttg ggtgtgaagt ncncttgc      540
ncataaccct ggaatatatt tgaaacagaa ctttttacca atcntttttt catgttaaaa      600
acnaaaattt t

```

611

<210> 179

<211> 611

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(611)

<223> n = A,T,C or G

<400> 179

```

acctcaattt tatcatttta gagtatttgt tagaatagga tctctccaaa atcaaacagg      60
atcaatctgg tcacgtctaa tcctaagaca aaacactatg taaaattttc ctgtatctaa      120
atgttgccct ctaggtaaat ctgtgatatt ttagagactt tcttttgtgg aaaaggtaat      180
ctgataaatg ggaagagatc atcagacaag ttcacaaata accattattt ctgcagaatt      240
cagttgaagt tggttttttt taaatgctta ttgggaattt ctaaagcact gacttggaga      300
ggccaagagc ctccatcaat ccctgcttgg atagccactc ccgttactac tgctaggtca      360
gggtctacag atgtgttggg atcttttcca aagaactctt gaatgacttg acggatccga      420

```

```

ggaataccaa tggagccccc aactaaaacc acctcatcaa tctcagtctt ttncagggtgg 480
nctttcttcaa tctcctgaat gggacctcgg ccgcancacn ctanggcgaa ttccacacct 540
ggcgcccgta ctaatggatc caactcgnac caacttgggg aacatggcta gtnttcnngg 600
ggaaatgttt c 611

```

```

<210> 180
<211> 621
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> '1)...(621)
<223> n = A,T,C or G

```

```

<400> 180
accctttaaac tggcaggaca tttttgaaat cacaaatttg cacataaaga atgtcacgaa 60
cagccatgta tccatataca gcaatcaaata aaggaactta tgacctaaag caaaggtaaa 120
ctttcttgaa acttaacatt ctataccaac taggcaacct ctgccagga tgagagtgg 180
atttttcaaa aacctctaata ttaatagtgc agcatttcgt tttccctgat ggctgtgtt 240
tcacagcagt ttttaaaaac tgcttggtca actatagctg cagcctatat cccagctatg 300
gaaaaaaaaaag taaatcttag ttcaattttt gccagttgtt tctgtattta aatttaaaaa 360
aaaacacact tccgctgggc aggttttagag ggttattatc aagtctgtgc ataactaaaa 420
gttcaaagca aattcaattt tgcttaangg aacattgnaa aagnacaatt cttggnanta 480
catgcctcgt tgatccattt naancatana aaattcaccc ttgtgtactg gttcaagaaa 540
aaaaccgatt tgacagttaa acatnttaaa anccccaacc tntgaagttc aaccaaactg 600
ganttttgtt cctcgccccga c 621

```

```

<210> 181
<211> 606
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(606)
<223> n = A,T,C or G

```

```

<400> 181
cgaggtacag accagagaca aagcaagaga agaagcagag actgttggcc cgggccgaga 60
agaaggctgc tggcaaaggg gacgtcccaa cgaanagacc acctgtcctt cgagcaggag 120
ttaacaccgt caccaccttg gtggagaaca agaaagctca nctgggtggg attgcacacg 180
acgtggatcc catcgagctg gttgtcttct tgctgcctct gtgtcgtaaa atggggggccc 240
cttactgcat tatcaangga aaggcaagac tgggacgtct agtccacaag gaagacctgc 300
accactgtcg ccttcacaca ggtgaactcg gaagacaaag gcgctttggc taaactgggtg 360
gaagctatca ggaccaatta caatgacnga tacnatgaga tccccctcct ggggtggcaa 420
tgtcctgggt ctaaatctgt ggcttgatn gccaaacttcn aaangcaaag cttaaaaact 480
tgcncttaac tngggtnaat gtactncccg gcggcgttg aanggcaatt caacacattg 540
cggccgteta atggntcanc ttggnccaac ttgggnaana tggnaaannn ttcttgggna 600
atttnn 606

```

```

<210> 182
<211> 610

```

<212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(610)
 <223> n = A,T,C or G

<400> 182
 ggtactcata aaaaaagtct tacccecaaaa ttgcaaacaa atacattaaa agattagaag 60
 aggtgataga aagcaccaga cattaacaaa aataaaaaata ataaaaataa ttcaactcaa 120
 aaggtcccca ttccagcaaat actttgtaaa gtatggcctg tatgtaaata gtgctaaatc 180
 aaggactttt tagcagaaaa ttgctcgggtt cttttatcta aggccttgaat ttgtaaagtg 240
 aaggcataaaa agttaccaaa cattaagtaa ctcttaaaat ggcacacagg ttttaaagct 300
 attgggtttt ccttcctaac tctctgaatt tttcccatgg cctttgtaga tcaactatct 360
 caaacgtatt ttacaccagc aactctcaac atacttgtct ttcagatatg tcatcagtca 420
 tgtctaacag gccaatagcc aaataacnga tttaaaacaa tnccttaacta gctagcagga 480
 cattactttg gatctgctta ctgcaactga ctatttgtta gcttaaaatc antttaatcc 540
 tgatacagaa acctcatctg cncatacatt actttggcct tcaaccttta aaaatactta 600
 atcccccgnc 610

<210> 183
 <211> 608
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(608)
 <223> n = A,T,C or G

<400> 183
 cgagggtactt tttttttttt tttttttttt tttttatctt tttttttttt tttttttttt 60
 tttttttggg agncagctnt ttaattaggn tcttaaaaca tttaaaacnc caatttgnga 120
 ggataaattc cattcgctc n ancaaacnca aatcgcaggt anccctggan ctgaggaata 180
 nctttgattt ttggnaaaat ttgngagtcc acagctttnt gatcaatntt gcncctgctcc 240
 gnaatctcat atttctnttt ttctgngncg aaaatctcac ctccctggng tntgggcttc 300
 cgcagcttnt tntttttgaa gtaagcatca ataaaangtt ttgggatttt tacattgctg 360
 aaatccattt tgggtgaagg ggcaatgaca aatttntngn gtnttctttt taaaagaacc 420
 tcattggggg ccnaaggncc cncceaaatt ataaacccct ttccccctgg tttangnaaa 480
 cccccctttg ccctgngggg nccangagga taaanaaagg ccccggggaa gctggcccca 540
 ntttttcccg ccgncgaagg gttttgccgg ctaaaanttt tngggcattt nnnnggnaat 600
 tttggctt 608

<210> 184
 <211> 622
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(622)
 <223> n = A,T,C or G

```

<400> 184
acagccctga tgcaaaagttt cagagcatga ccagcaagtg gccagctgtg tgggtcaaga      60
tcagctccag ctgggtctgc ctctgtcttt acgtctggac ccttgtggct ccacttgtcc      120
tcaccagtgc ggacttcagc tgaacctctg agtgccaagg acaccactgg aactcacaaa      180
ggtctccttc accgaaaacc catatacctt ttaagtttgt ttcaactaaa atattaagtg      240
aatgctttgc aagtttgact gtatgcaggt ttatatcaag aagggtgagat tgaataatgc      300
ttgatgcaga atcgaaactt ctcatattat tgnatattat gtttacttct aaggatatag      360
caciaaggga acattttttg tttaaaagtga actacagctg tgctgtgaag agagttcttt      420
ataaagcctg taggtctttt aactttggtt aaaatgtaag ataggaaaaat gttggatatt      480
tgaggcntgc ctaatatatt tatattggag natccttttna aagccaaaaa aaaaaaaaaa      540
aaaaaaaaagt nccttggccg gaccncccta aggggaattc cacncaactgg gggccgtntt      600
atggatccaa ctcgnaacca ct                                     622

```

```

<210> 185
<211> 614
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(614)
<223> n = A,T,C or G

```

```

<400> 185
acgcgggggac agtcccaccc tcacacgatt ctttaccttt cacttcatct tgccttcat      60
tattgcagcc ctagcagcac tccacctcct attcttgcac gaaacgggat caaacaaccc      120
cctaggaatc acctccatt ccgataaaat caccttccac ccttactaca caatcaaaga      180
cgccctcggc ttactttctc tcctttcttc cttaatgaca ttaacactat tctcaccaga      240
cctcctaggc gaccagaca attataccct agccaacccc ttaaacaccc ctccccacat      300
caagcccgaa tgatatcttc tattcgccta cacaattctt cgatccgtcc taacaaacta      360
agaggcgctc ttgccttatt actatccatc ctcatcctag caataatccc atccttcata      420
tatcccaaca acaaagcata atatttcgnc cactaagcca atactttatt gattctagcc      480
ggagacctct nantntaacc tggatcggag gaaaccagta gctacccttt accaatantg      540
ganaagaaga tcgnaccttg gcgggacacc ttangngaatt tcaaccactg gnggcggtat      600
atgggacccn ccng                                           614

```

```

<210> 186
<211> 627
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(627)
<223> n = A,T,C or G

```

```

<400> 186
ggtactgatt ttaaaaaacta ataacttaaa actgccacac gcaaaaaaga aaaccaaagt      60
ggteccacaaa acattctcct ttctttctga aggttttacg atgcattgtt atcattaacc      120
agtctttttac tactaaactt aaatggccaa ttgaaacaaa cagttctgag accgttcttc      180
caccactgat taagagtggg gtggcaggta ttagggataa cattcattta gccttctgag      240
ctttctgggc agacttgggt accttgccag ctccagcagc cttcttgtcc actgctttga      300

```



```

tgacacccac cgcaactgtc tgtctcatat cacgaacagc aaagcgaccc aaaggnggat 360
agtctgagaa gctctnaaca cacatgggct tgccaggaac catatnaaca atggcagcat 420
caccagactt naagaattta agggcatctt ccacttttta ccaaaacngn gaacaatctt 480
tttcttact taacnaacnt gcttccatgg gagccggng naatccaatc aagggcataa 540
cccgggcctt atttggcnng atgggtcang gnaatancct gaccaggaaa cccctgnttc 600
cttgggggga antttgttgn nccccac 627

```

<210> 187
 <211> 256
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(256)
 <223> n = A,T,C or G

```

<400> 187
ggaccttttt tttttttttt tttttttttt ggaaaagaaa ggccttacat atttattact 60
gaatccagcc aaccaacgtg ttcataacag attcagagag gaaaacacgt cgaaatctcc 120
anatagttgt gacattttca gcttgatatt gtaacatgat cgtgaccttc anacagcata 180
aatatgtgtg ccattctcat tgcaattcct tatanacca gcttggttct tctccaatgt 240
ctccttttgg agttgt 256

```

<210> 188
 <211> 523
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(523)
 <223> n = A,T,C or G

```

<400> 188
ggtaccacct acaccaaca agtcaatgag ggacttcttt ttaatttggt aggattttga 60
ctggttttgc aacaataggt ctattattag agtcacctat gacaaaaaat aggggttacc 120
tagataatgc caaagtcagc atttgtcctg gggtcccttg tgtgatctgt ttggactatg 180
ttttcttttc ttctccact tgctcagcag cttgggcttc cattctagct cttttaccaa 240
gatttttgtg tgaccatgtt gacttcattt ggattgccct ctttcaattt ccttgtgaaa 300
acacccttaa ctttctcttt acccttagct gaaatgttta cataacttct ggtgatattc 360
tttcatgatt ttatatctct taaaatgggt atggatgtga cacctcataa aagtgagctt 420
tgaactgtag ataactctta aagaaaatgt cattttanac aattaaaata tttgtgctca 480
aaaaaaaaa aaaaaaaaaa gtcctgcccg gcggccgtcn aan 523

```

<210> 189
 <211> 622
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(622)

<223> n = A,T,C or G

<400> 189

```

acaatttaaat ttttctgctt gcccaagaaa caaagcttct gtggaacat ggaagaagat    60
gaaaatgaga ctggcaaaga acaaatgctg aatctgaaga agaggacaac tttgggcaaa    120
taatctgcat acttttaatt gggaataaga tggaaaatat gaatgctaaa tcaaattttt    180
taaaaaatac accacacgat acaactcaat acaggagtat ttcttctcaa attcttctag    240
caccatcaac attcttcaag tatctgaaat actattaatt aagcaccttt gtattatgaa    300
caaaacaaaa caaggacctc agttcatctc tgtctaggctc agcacataac aatgtggatc    360
acactcatgg gaaagtgttt tgaggtagtt taaacctttt ggaagggttg gttttaaact    420
tcctctctgtg gaagatatca aaagcccaa gtggtgccaa atggttatgg ttttattttt    480
caatttttaat ttgggtttct tccaaagggt acatccccat acaaggggaa ggggggtggaa    540
aaaaaatcaa attttggggg accagggagg ataatnaact gtttgcaatg cttgacaacc    600
tttttttttt gnccaantaa ca                                     628

```

<210> 190

<211> 628

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1) ... (628)

<223> n = A,T,C or G

<400> 190

```

accactaata ggggtgtatct cagaaactga attgaaataa gggaaaatag gattttctgt    60
cctgggtttt gaagattgtt cttgattccc ttgattccca ggagagattc tctgacattc    120
acgtgtcagc cactttggca cggaagcctt acagtgtggg gaacccaaaac ttcgtgtctc    180
ctctttcccc gatgccatca gcatagactt gacttcctta aaccgagagt tttgatgtgg    240
ccttggaac cctaaaatca gctgtgtag gtaacaaaac tcaggctttc tgttgatgac    300
atcgagatgg tgtaacttaa aagagccaag attcctgttt tcagtttgtg gattcatcct    360
gctgggttta ctttagtccc tccatgtcaa agtgggcctg agaaaagctc atacatgcct    420
catgtgaagt gtccaccccc tctgaaaatc tttcttgttc aaaacancna cgacatatct    480
tggtaaactt tacggtgact tttggangag gggagtttg aaattgtaaa atgttatana    540
tggtgcctat ttctgtctga angaaatgtt ttaaaaagnn tntntaancn taatcnaatg    600
gttggggggg gaccttctac cnaanntn                                     628

```

<210> 191

<211> 474

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1) ... (474)

<223> n = A,T,C or G

<400> 191

```

ggtacagccc tcaatctgtt cttcaagctc aagaacttca agacagctgc cacctttgct    60
cggcgcttac tagaactcgg gcccaagcct gaggtggccc aacagacccg aaaaatcctg    120
tctgcctgtg agaagaatcc cacagatgcc taccagctca attatgacat gcacaacccc    180
tttgacattt gtgctgcac atatcgcccc atctaccgtg gaaagccagt agaaaagtgt    240

```

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ccactcagtg gggcctgcta ttcccctgag ttcaaaggtc aaatctgcag ggtcaccaca      300
gtgacagaga ttggcaaaga tgtgattggg ttaaggatca agtcctctgc agtttcgcta      360
aagccccctt tgtgtgcatg ggtcaagtca ccatatgttc cccccaaaaa atgtgtctat      420
atctccttct aacaacacct tcccctgcac tactcttcaa atctnctct ntgt              474

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<210> 192
<211> 234
<212> DNA
<213> Homo sapiens

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```

<400> 192
acgcgggggt tttgtgagtg gctcctaccg accgaggttt aggcagcgcg gggagctttg      60
cgggttgcca tttgtaactc cggatcctaa aattcctgtc ctgttctctg tctcttctag      120
gttggggggc gtcccgtctc taaggcagga agatgggtggc cgcaaagaag acgaaaaagt      180
cgctggagtc gatcaactct aggtcccaac tcgttatgaa aagtgggaag tacc              234

```

```

<210> 193
<211> 367
<212> DNA
<213> Homo sapiens

```

```

<400> 193
ggtaccaata ccaccaattt tgtagacatc ctggagaggc aggcgcaagg gcttgtcagt      60
tggacgagtt ggtggtagga tgcagtcacg agcctcaagc agcgtgggtc cactggcatt      120
gccatcctta cgggtgactt tccatccctt gaaccaaggc atgttagcac ttggctccag      180
catgttggtc caattccaac cagaaattgg cacaaatgct actgtgtcgg ggttgtagcc      240
aattttctta atgtaagtgc tgacttcctt aacaatttcc tcatatctct tctggctgta      300
gggtgggtca gtggaatcca ttttgttaac accgacaatt agttgtttca caccagtg      360
cccgcgt

```

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<210> 194
<211> 613
<212> DNA
<213> Homo sapiens

```

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<220>
<221> misc_feature
<222> (1)...(613)
<223> n = A,T,C or G

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```

<400> 194
ggtactcttg gtttgtcaat gggactttcc agcaatccac ccaagagctc tttatcccca      60
acatcactgt gaataatagt gqatcctata cgtgccaaag ccataactca gacactggcc      120
tcaataggac cacagtcacg acgatcacag tctatgcaga gccacccaaa cccttcatca      180
ccagcaacaa ctccaacccc gtggaggatg aggatgctgt agccttaacc tgtgaacctg      240
agattcagaa cacaacctac ctgtgggtggg taaataatca gagcctccgg tcagtcccag      300
gctgcagctg tccaatgaca acaggaccct cactctactc antgtcacia ggaatgatgt      360
aggaccctat gagtgtggaa tccanaacga attaagtgtt gccacagcga cccagtcatt      420
ctgaatgtcc tctatgncca gacgaacccc catttcccct cataccctan taccgtcaag      480
ggtgaacctt agctttctgc atgcagcttt aaccactgcc agtttcttgn tgatgatgga      540
catcacacca cacaagactn ttatttcaca tactgagaan aaagcgactt ntactgcagg      600
cataactanc ngg

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<210>	198
<211>	539

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<212> DNA
<213> Homo sapiens

<400> 198
cgaggtacta catatttcag cactaaggcg gttgcttcac tttatatcta tataaaaaaa 60
gtggtaaaaa tcttttcctt ttgtgcagtt gaacccatcc tacattcaga ttctctcaag 120
cactaataaa atacttatatt ggttgaggaa gatttaaggc aagttcgggc ccttccaaag 180
gcactgtgag actccccccc cactccccgt tattgtctaca tgtctttata ctcgagtatg 240
tcacagtaga actgggtggaa taagcaaaca cttttttgct agtttataaa gttggaatta 300
gaaaagcatg ccacatttca gcctgattgc aaagtatgtg gtcatttttt tctttgaagt 360
tggatgggct acaaccttta tacattctaa gaaaactcat aggatgttcc tcaaactact 420
tccacagcat caagatcgat ttctgtcaag aaatcatgca atctttcaaa atttacgtaa 480
acaaggaaag aaattaatga aataaatatt acatacaatc tcttaaatta agaatttgt 539

<210> 199
<211> 626
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(626)
<223> n = A,T,C or G

<400> 199
cgaggtacaa gatgtccaaa tattgcgaag atctattttgg ggatctcctg ttgaaacaag 60
cacttgaatc acatccactt gaaccaggca gggctttgcc atcccccaat gacctcaaaa 120
gaaaaaatac cataaaaaaac aagcggctga aacctgaagt tgaaaaaaa cagctggaag 180
ctttgagaag catgatggaa gctggagaat ctgcctcccc agcaaacatc ttagaggacg 240
ataatgaaga ggagatcgaa agtgctgacc aagaggagga agctcacccc gaattcaaat 300
ttggaaatga actttctgct gatgacttgg gtcacaagga agctgttgca aatagcgtca 360
agaaggcttc agatgacctt gaacatgaaa acaacaaaaa gggcctgggtc actgtagaag 420
atgagcaggc gtggatggca tcttataaat atgtagggtc tccactaata tccatncata 480
tttgccaca atgatcaact acgcccacct gtaaaagggtc aagggttncat gtggcagaag 540
aaccncatat tcattataca tggcttcttt tatgaatant cggccttggt tcttgaancc 600
cttgcaatga atttgnaatt ntacca 626

<210> 200
<211> 618
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(618)
<223> n = A,T,C or G

<400> 200
actcataaaa aaagtcttac cccaaaattg caaacaaata cattaaaaga ttagaagagg 60
tgacagaaaag caccagacat taaacaaaat aaaaataata aaataaattc aactcaaaag 120
gtccccattc agcaaatatt ttgtaaagta tggcctgtat gtaaataagt cttaatcaag 180
gactttttag cagaaaattg ctcggttctt ttatctaagg cttgaatttg taaagtgaag 240
gcataaaagt taccaaacat taagtaactc ttaaaatggc acacaggttt taaagctatt 300

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<210> 203
 <211> 577
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(577)
 <223> n = A,T,C or G

<400> 203
 ggtactttttt tttttttttt tttttttttt tttttt ttt tttttttttt tgaaaaagtc 60
 atggaggcca tggggttggc ttgaaaccag ctttgggggg ttcgattcct tccttttttg 120
 tctaaatttt atgtatacgg gttcttcnaa tgtgtggtag ggtggggggc atccatatag 180
 tcaactccagg tttatggagg gttctttctac tattaggact tttcgcttcn aagcgaaggc 240
 ttctcaaatac atgaaaatta ttaatatattac tgctgttaya naaatgaatg ancctacaga 300
 tgataggatg tttcatgtgg ggtatgcata ggggtantcc gagtaacgtc ggggcattcc 360
 ggataggccn agaaagtgtt ntgggaanaa agttagattt accccgatga atatgatagt 420
 gaaatggatt ttggcgtagg tttgggtctag ggtgtancct gagaataggg gaaatccgtg 480
 aatgaaacct cctatgatgg caaatacact cctattgnta ggacataatg ngaagtgagc 540
 tacaaccgta atacctgccc nggcnggccc ttannan 577

<210> 204
 <211> 629
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(629)
 <223> n = A,T,C or G

<400> 204
 cgaggtaactt gttttttttt ttttttttga gacggagtct cagtctgtca cccaggctag 60
 agtgacagtgg cagcacatcg gctcactgca acctccgcct cccgggttca agtgattctc 120
 ctgcctcaac ctcccagta gctgggacta caggcatgtg ccaccacgcc tgactaattt 180
 ttgtattttt agtanagatg ggatttcatt atgttggcca gctgggtcttg aacttctgag 240
 ctcaaggatg ccaccgcct tagcctncca gagtgcctagg ataacaggca tgagccgtcg 300
 cgccctggcca aaatagcata atgttttaag aaagtttacg aatttgtctt gggccacatt 360
 naaaaccatc atggggccaag gggttgacaa gctagcctta ggtcatgtca gaatgcaatt 420
 taacaggaat ttcaagcnaa acttacaaaa aattaaatcc acaaaaaaaaa tatcatttgg 480
 taaatgcact gnctacacac tttactncta agtccattca accatgacga ccccttacct 540
 aaaaattagg gcattctccc aagttctaaa gatgatttct aaaacattac caangnctaa 600
 agtctaattc ccacaaanct ttttttttn 629

<210> 205
 <211> 424
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(424)

<223> n = A,T,C or G

<400> 205

ggtacaaatg	cttttatatt	cagccctgt	aaagccatca	gatgtttgaa	agttttttaa	60
cacgaaccaa	agggtttaat	tttaagaact	tagctaggaa	tgggtgaaat	cctacccaat	120
taatagagtt	ctgcaaatta	gtaacaaagt	gtaaaatgaa	aggaagggtc	ccttgagat	180
gtgaaattct	tctattgaga	gtcctgtctt	ctttattcaa	gaagtttgta	gccattttca	240
gaattcactc	agaaccaaac	ttcttaattt	agatatcagc	gaacaagtca	tggcaaaaaa	300
tacacaaaga	gaaacaccac	cacatcgaaa	aggatgaaaa	gccagaggtc	caaccagtan	360
gagtgtttgg	gaagcccatt	tgccccagac	tgaggcctca	catcgaagtt	ctgcctcccc	420
gcgt						424

<210> 206

<211> 633

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1) ... (633)

<223> n = A,T,C or G

<400> 206

ggtaccaatg	gtgcctcctg	gaatcaagta	tctttacctt	aggaataacc	agattgacca	60
tattgatgaa	aaggcctttg	agaatgtaac	tgatctgcag	tggctcattc	tagatcacia	120
ccttctagaa	aactccaaga	taaaaggag	agttttctct	aaattgaaac	aactgaagaa	180
gctgcatata	aaccacaaca	acctgacaga	gtctgtgggc	ccacttccca	aatctctgga	240
ggatctgcag	cttactcata	acaagatcac	aaagctgggc	tcttttgaag	gatttggtaaa	300
cctgaccttc	atccatctcc	agcacaatcg	gctgaaagag	gatgctgttt	cagctgcttt	360
taaaggctct	aatcactctg	aataccttga	cttgagcttc	aatcagatag	ccagactgcc	420
ttctggcttc	cctgtctctc	ttctaactct	ctacttagac	aacaataaga	tcagcaacat	480
ccctgatgaa	gtatttcaag	cgtttaatgc	tttgagtagt	ctgcgtttat	ctcacaacga	540
actggctgat	agtggaatac	ctggaaattc	tttcaatggn	gccatcctgg	gtgaacctgg	600
acttgcctat	accagcntaa	aacataccac	cgg			633

<210> 207

<211> 623

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1) ... (623)

<223> n = A,T,C or G

<400> 207

ggtacttttt	tttttttttt	tttttttttt	ttagaaacta	tggctcttta	ttttcatgtg	60
gataattcaa	acaaagtcac	tagtagtctt	tgttcaattt	tttttttaaa	aacaaaaaaa	120
ccctcaaata	aaaaatcttg	ggcttaaaag	aactctatca	caggagcctg	gttgaggat	180
tcctagtttt	atacatgaga	aatagaatgc	agatttctct	gaagagtgtt	taaagaagga	240
atggtagtgt	agggggctta	tttcccaggc	tcaaaagtgc	ttaggggtgg	tgccacagt	300
ctaggtatag	ggtgatggac	agtgatcact	gccgagggcc	ttggaacgga	tcttgctgtc	360
acacaatgca	ggtaacagag	agtgggacaa	caaaaagtaa	tcaaggcgcc	aaccaacatt	420

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cttggatcga gcattcatat ataagtccaa aaggtgtang cataaggtgt gttgggggtan 480
aagtgcctaa agctgcaacc agtggcacan cctgcagtaa ttccccgaac cttggccttt 540
tggggcgtga anccnccatt cttttggtnc cctnggggtg cnaaggcaat ttttnatgtg 600
cccattgagg gttcaaacac aca                                     623

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<210> 208
<211> 620
<212> DNA
<213> Homo sapiens

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<220>
<221> misc_feature
<222> (1)...(620)
<223> n = A,T,C or G

```

```

<400> 208
acgatgtcta gtgatgagtt tgctaataca atgccagtca ggccacctac ggtgaaaaga 60
aagatgaatc ctagggtctca gagcactgca gcagatcatt tcatattgct tccgtggagt 120
gtggcgagtc agctaaatac tttgacgccg gtgggggatag cgatgattat ggtagcggag 180
gtgaaatatg ccccgcgtag ttgctttgaa agattaccta ctattttatg ataaaatgta 240
gttgtctcca gagcttaaat ataatttgta aagcacttgg tttaaaatttc tctctaccta 300
taaacagttt agcattaagg gtttctatta atgacacaga attattggcc aagtgttaatt 360
tcttaaaatt tagcattact ttaaatagcc agcatgtaat acaagtaact acactacctc 420
atatctacat gattttcaag ttgtaatgca gatggacaga taaaaaagat ttacgttgnc 480
ttttggccat aagtgggaaa agttttctgn atattgcata gcattacaca tttatgccta 540
ttttacatta acttctaaag aagtttttct aagaaaangg ttcaggcaat attttttgag 600
gctgccgaan aaaaatgant                                     620

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```

<210> 209
<211> 624
<212> DNA
<213> Homo sapiens

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<220>
<221> misc_feature
<222> (1)...(624)
<223> n = A,T,C or G

```

```

<400> 209
ggtactggta caaaaacagg cacataaacc aatgaaacag aatagaaagc ccagaaataa 60
tgcttcaccc ccacaacccat ctgatcttca acaaaaataaa caaaaacgag ccatggggaa 120
aggactccct attcaataaaa tgggtgctggg ataactagtt aaccatatgc agaagattaa 180
agctggaccc ctcccttaca aaataaggag c*ggaccctt tatacaaaaa tcaactcaag 240
atggattaaa gccttaaatg tgaaactata aaaccctgga agacaacata ggcgattcca 300
ttctagacat cagaactggc aaagatttca tgaggaagac accaaaagca attgcaacaa 360
aagcaaaaat tgacaactgg gatataatta agtttaagag cttctgcaca gcaaaagaga 420
gactatcagc agagtaaaca gaccacctac agaatgggag aaaatatattg caaactatgc 480
atgtgacaaa ggtctaatat ctagcatcta taagtactta aacaaatttc aacagaaaac 540
caacacccca ttaaaaagtg ggcaaggaca tgaacaaatg cttttcaaaa gaagacatct 600
gcttntacag tttntgaaac aaag                                     624

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```

<210> 210
<211> 504

```

<212> DNA

<213> Homo sapiens

<400> 210

acgcggggca	gctagcagat	gcttttaggac	ctagtatctg	catgctgaag	actcatgtag	60
atattttgaa	tgatttttact	ctggatgtga	tgaaggagtt	gataactctg	gcaaaatgcc	120
atgagttctt	gatatttgaa	gaccggaagt	ttgcagatat	aggaaacaca	gtgaaaaagc	180
agtatgaagg	aggtatcctt	aaaatagctt	cctgggcaga	tctagtaaat	gctcacgtgg	240
tgccaggctc	aggagttgtg	aaaggcctgc	aagaagtggg	cctgcctttg	catcgggggg	300
gcctccttat	tgcggaatg	agctccaccg	gctccctggc	cactggggac	tacactagag	360
cagcggttag	aatggctgag	gagcactctg	aatttggtgt	tggttttatt	tctggctccc	420
gagtaagcat	gaaaccagaa	tttcttcact	tgactccagg	agttcagttg	gaagcaggag	480
gagataatct	tgcccaacag	tacc				504

<210> 211

<211> 619

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(619)

<223> n = A,T,C or G

<400> 211

accatgaaat	atccagaaca	tacttatatg	taaagtatta	tttattttgaa	tccacaaaaa	60
acaacaaata	attttttaaat	ataaggattt	tcctagatat	tgacggggag	aatatacaaa	120
tagcaaaatt	gaggccaagg	gccaagagaa	tatccgaact	ttaatttcag	gaattgaatg	180
ggtttgctag	aatgtgatat	ttgaagcacc	acataaaaaat	gatgggacaa	taaatttttg	240
cataaagtca	aatttagctg	gaaatcctgg	atttttttct	gttaaactctg	gcaaccctag	300
tctgctagcc	aggatccaca	agtccttggt	ccactgtgcc	ttggtttctc	ctttattttc	360
aagtggaaaa	agtattagcc	accatcttac	ctcacagtga	tggtgtgagg	acatgtggaa	420
gcactttaag	ttttttcacc	ataacataaa	ttattttcaa	gtgtaactta	ttaacctatt	480
tattatttat	gnattttatt	aagcatcaaa	tatttgtgca	agaatttgga	aaaatagaag	540
atgaatcatt	gattgaatag	tattaagatg	tatagtaaat	tattttattt	ananattaaa	600
ngangtttat	taganaaan					619

<210> 212

<211> 479

<212> DNA

<213> Homo sapiens

<400> 212

cgagggtaca	agcagcaact	gcaatactca	agggtaaaac	attagaaaag	catttgtgtg	60
acagggtatat	tacagtatta	tcaaaatatt	acatttttcag	acttacttag	cagataatca	120
tccaccagag	cttaaatctt	taaattattt	ccatagctct	aaaaaatatg	taatgtcaga	180
atgcatataa	aaagaatgta	aaaggaaacc	taaaatacaa	atggaataat	gtaacaaata	240
aatatttgat	ttcagtaact	gttaataatc	agctcaacac	caccattctc	tctaaactca	300
atttaattct	tataggaata	atgaactgtc	aaatgccatg	gcataattat	ttattttccaa	360
gctatcatca	atgattagaa	ctaaaaaaat	tttggcataa	aaaaatcaca	attcagcata	420
aataaagcta	tttttagctt	caacactagc	tagcatctct	aagaattgtt	gaaataagt	479

<210> 213

<211> 487
 <212> DNA
 <213> Homo sapiens

<400> 213
 actgtttact gcctgggcac tatactttct atgcagatct cctttgtggg tttccagcct 60
 gtcctttcat cagagcacat ggcagccttt ggggtctttg gtctctgcca gatccatgcc 120
 tttgtggatt acctgcgag caagttgaat ccacaacaat ttgaagttct tttccggagc 180
 gtcattcttc tggtaggctt tgtccttctc accgtgggag ctctcctcat gctgacagga 240
 aaaatatctc cctggacggg gcgtttctac tctactgctg atccctctta tgctaagaac 300
 aacatcccca tcattgcttc tgtgtctgag catcagccca caacctggtc ctcatactat 360
 tttgacctgc agctcctcgt cttcatgttt ccagttggcc tctattactg ctttagcaac 420
 ctgtctgatg cccggatttt tatcatcatg tatggtgtga ccagcatgta cctcggccgc 480
 gacacgc 487

<210> 214
 <211> 393
 <212> DNA
 <213> Homo sapiens

<400> 214
 cgaggtacaa tatgctgcag cataatattgt caggccaacc ttcacaccat attttggcag 60
 ttctgttgca tacgctgcgc agactatcat atccccctct atacgggcat aagcaatctg 120
 acaaatgata tctctgtttg tcacacgaac tatcatcctg tatttgggtg tgttgtattt 180
 atttttatct tgtatcacca agcgtttccg agcataataa tcagttttac cctctcgtcg 240
 tctttctaaat ttcaacttgg atctcttaaaa gtaggcctta ttcttaacaa ctttaacaaa 300
 ccccatcctg cggaacagag accggcgctc gctgctcgac agagacctgc aggcccagcg 360
 gcgctagggg gtgggaaaag ggccaccccc cgt 393

<210> 215
 <211> 615
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(615)
 <223> n = A,T,C or G

<400> 215
 ggtacagtaa caagtgttgg cattatcagt tgaactgtaa atacaaaatg cttcttccaa 60
 ttagtctcta tgatgattaa gtttctaaaa tttatcrgaa caccattcag aaacttgttt 120
 tggggaattt gatagttatt gatgtgcac tggtaaactg atgacagaca taactcatca 180
 ttccccagaa accttttttg attacagtac ctaacatttt gcctcctctt ttttggtttt 240
 gctgggtata aaggtttggg ttggagaggg ctactggat cccaatcctt ggagctggat 300
 cattggattc aaatcataat gtggatagga tagggaggat gaattaccag gattcatgga 360
 gcgggatcag attaccagga acataggagt ggattcctgc ccaaccaaac ccgcattcgt 420
 gtggattttt ttattcaact taattggcta ttocaaagat ttttttttcc tatttttgac 480
 gaatggagcc cttaagatgc acgatggaat tgggtttgag ttttttggtaa aaggaccaaa 540
 ccaggcctgg agataacgct ggagcaatct cntggaagga ttagccccaa ttgatgggaa 600
 catttaangg ggaag 615

<210> 216

<211> 322
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1) ... (322)
 <223> n = A,T,C or G

<400> 216
 ggtacttttt tttttttttt tttttttttt ttttttggag ttgtaggcaa atgtttaatt 60
 aattctgctc atatgcacat ctgaaagcat gagacacact ccacagacag cagcactggt 120
 ggctgggtgg gcanatgggc actcgccgat taggtattaa tgtcaataat acgtgcataa 180
 agtgctgata aaataactta agtgttacaa aaagagacag tccacgggtg ctgcaggcac 240
 atgcaggcgg gactgggtca aacactccag ggctgcacat gttccagctg gcctgagtcc 300
 gacacgtcat aactggcctt gt 322

<210> 217
 <211> 606
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1) ... (606)
 <223> n = A,T,C or G

<400> 217
 acgcgggggg aagtgagcga cacactctgc gtcctogcct caccagagtc ttgctgtgtg 60
 gcccaggctg gagtgcccgg ctggtctcaa attcctgacc tcaagtgatc tccctcccaa 120
 agtgttgcga ttgcagggtg gagccactgc acctggctgc tgagaaatct ttgcctacag 180
 tgagggaaac tactaaagtt cctggggaag caaagtaaga atttcataag aacaaaatgg 240
 atggagagga gaaaacctat ggtggctgtg aaggacctga tgccatgtat gtcaaattga 300
 tatcatctga tggccatgaa tttattgtaa aaagagaaca tgcattaaca tcaggcacga 360
 taaaagccat gttgagtggc ccaagtcaat ttgctganaa cgaaaccaat gaggncaatt 420
 ttagagagat ccttcacatg tgctatcgaa agtattcatg nattttacgt accttgggcc 480
 gcgaccacct taaggccaat tncacacact ggcnggccgt actantggat ccnactngga 540
 ccaacttggc gtaatcatgg catactgggt cctggggaaa atgtatccgt tacaattcnc 600
 acacan 606

<210> 218
 <211> 618
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1) ... (618)
 <223> n = A,T,C or G

<400> 218
 ggtacttttt tttttttttt ttttttttga gacggagttt ggcccttggt gcccaggctg 60
 aagtgaata gtgcgatctc ggctcactgc aacctccacc ttccgtgttc aaccgattct 120

```

cctgcctcag cctcctgagt agctgggatt acagatgaaa aaacatttaa agcccttaag 180
gaagaaggaa atcaatgtgt aaatgacaaa aactataaaag acgcccctcag taaatacagc 240
gaatgcttaa agattaacaa taaggaatgt gccatatata caaacagagc tctctgttac 300
ttgaagctgt gccagtttga agaagcaaaag caggactgtg atcaggcact tcagctagct 360
gatgggaacg tgaaagcctt ctatagacga actctggctc ataaaggact caagaattat 420
cagaaaagct taattgatct caataaagtt atcctactag atccaagtat tattgaggca 480
aagatggaac tgggaagangt aactagactc ctaatcttaa ggataagaca gcaccattca 540
acaaagaaaa ggagagaagg aaaatgagaa tcaagaggng aatgaaggca ngaggancct 600
ggaaaacctg aggggagg 618

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<210> 219

<211> 613

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(613)

<223> n = A,T,C or G

<400> 219

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ggtacaaagc ggatctgagc ccggaaaatg ctaagctcct cagcacattc ctaaattcaga 60
ctggcctaga cgccttcctg cttagagctgc acgaaatgat aatcttgaaa ctaaagaacc 120
cccaaaccce aaccgaggag cgcttccgcc cttagtgagg cctgagagac actctcgtaa 180
gttacatgca aactaaagaa agtgaaattc ttcttgaaat ggtatctcag ttcccagaag 240
agatactgct cgccagctgt gtctcagtgt ggaaaacagc tgctgtgctg aaatggaatc 300
gagaaatgag atagaattat ttctcagct atctttggat gactttggag agaagactcc 360
tctctcctcg tctgcggcgt ggacttgatc atggactggg gcctttgcat tcagaaggag 420
agctgtcagc gtagcaccga attcaagacc aaggcgtgct acctgagctg acagcttttt 480
gaaagccgag ctggttctga accatgtcct gccnngcng gcgctcgaaa gggcgaaattc 540
agccactggc ggccgtacta ntggatccga actcggacca aacttggcgt aatatgggca 600
tactggttcc tgg 613

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<210> 220

<211> 616

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(616)

<223> n = A,T,C or G

<400> 220

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ggtacgcggg ggcagccgcg gtgtttgtgct gtggggaagg gagaaggatt tgtaaaccce 60
ggagcgaggt tctgcttacc cgaggccgct gctgtgcgga gacccccggg tgaagccacc 120
gtcatcatgt ctgaccagga ggcaaaacct tcaactgagg acttggggga taagaaggaa 180
ggtgaatata ttaaaactcaa agtcatttga caggatagca gtgagattca cttcaaagtg 240
aaaatgacaa cacatctcaa gaaactcaaa gaatcatact gtcaaagaca ggggtgttcca 300
atgaattcac tcaggtttct ctttgagggg cagagaattg ctgataatca tactccaaaa 360
gaactgggaa tggaggaaga agatgtgatt gaaagtttat cangaacaaa ccgggggtca 420
ttcaacagtt tanatattct ttttaattnt ttcttttnc tcaatccttt tttattttta 480
aaaatagttc ttttgtaatg tgggtgtcaaa acggaattga aaactggcac cccatctttt 540

```

gaaacatctg gtaatttgaa tetaatgctc attatcatta tggttggttt cattggcnga 600
 attttgggga tcaanc 616

<210> 221
 <211> 615
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(615)
 <223> n = A,T,C or G

<400> 221
 ggtacagtga tagctcccc tgggcaatac aatacaagaa cagtggggtt tgtcaaattg 60
 gaacaaggaa acagaaccac agaaataaat acattgggta acatcagatt agttcagggt 120
 acttttttgt aaaagttaaa gtagagggga cttctgtatt atgctaactc aagtagactg 180
 gaatctctctg tgttcttttt tttttaaatt gggttttaatt ttttttaatt ggatctatct 240
 tcttccttaa catttcagtt ggagtatgta gcatttagca ccaactggctc aatgcgctca 300
 cctaggtgag agtgtgacca aatcttaaag cattagtgtc attatcagtt accaccattt 360
 ggggctttta tcttcatgg gttatgatgc tctcctgatg acacatttct ctgagttttg 420
 taattccagc caaagagaga ccattcacta tttgatggct ggctgcatgc agacatttaa 480
 agctttttaga gaatacacta caccagggag tatgactact antatgacta ttagganggt 540
 aataccaga attggactcg caccttaggc aagatccaac cactaaattg aataagaatg 600
 agtngatgag gtncc 615

<210> 222
 <211> 617
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(617)
 <223> n = A,T,C or G

<400> 222
 ggtacttttt tttttttttt tttttttttt ttttaattta tgatttttatt gncttttctt 60
 tgtccggcct ttaacatggt tctgtaattt aaataaaaaat ctattttactt tctccatttt 120
 agcaaatggg ttcttttacc aaatagggtg cactatagtc cccatattgtt tttctactgn 180
 tccacaacca ctatttcaca aagattgaca aaactttaat aaaagttaaa tttacagaca 240
 tcttaagata acttgggaaa tatgtagtaa aaaagaatcg agtccacaaa ttaagaatat 300
 tttgctaata tgcccaacac caatttcagc aaatccaatc tacttaactc atatatttaa 360
 tngngtaatt tttctaacaa aatttaattg gggtatgaat gatataattt tgcccttgac 420
 aaagatgaca tgtgtgattt tgggtngact aanaaaggag aagtatgatt tctggngggg 480
 atganatcac tctggctcat cgaagctcca gaatatgtaa gggctctgnca cgtccaaaaa 540
 tgttaggcna atgtataaaa ggccaccggg ctnacacacg ttttatatac aaactttngn 600
 agtccctttta tntcata 617

<210> 223
 <211> 470
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(470)
 <223> n = A,T,C or G

<400> 223
 ggtaccacaa ctgtgccctt gataattagt aatcactcct aaaaatcttc atttggcacc 60
 agatgggtgtg tttaaaacac cctaggatgt tttgaatcag gcttgatttt gttagttgag 120
 ttacaggaga attttaaggg tgaggggatg ggggtcaggg aagaaaagga aatgggaaat 180
 ggaccagaaa aaatcttgag tcatcatcta aatcaacaaa gcactgatag ctccaaatat 240
 taggtcagac actaaaacga ctgatatagg ctcaagtggg ttataaaaacc tataaaaaga 300
 ctacaccagc aaagtccctg tcaatctgtc agagttcaga aactaaaaca gggagtaaca 360
 ttttagctta aaaccttatc tcaagagaat catatacact tcacatgaat aaaaatacct 420
 gaaaccaaac atttttataaa gctccagtcg tgcccnnggc ggccgctcga 470

<210> 224
 <211> 622
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(622)
 <223> n = A,T,C or G

<400> 224
 gcgtggncgc ggccgacgtn ctcttttttt tttttttttt ttttttgenn actaaaaatn 60
 ngattgctct ttaaagcctt aggccgnatg acaaaatgan nagactgaaa tgacancggg 120
 gaggaagaaa cagannaaag ataagaatga ggtgggtcagg ttgggggaat taagcgaata 180
 ttcncttccn nggtgagtc tncactggg ctcatgccca tgatgagttg tacaccaaac 240
 acnggctgnt gacttncctc ctgcnctant cagtgaactt gcngacatng ggnancctca 300
 cattacagnt ataanntttc cacctaaaaa atgctgcgct tttcgacnng ctcnncnagn 360
 ggccgggggct tgacatggng gaanggattt ctctcccatg ccaaggaatt catcacatca 420
 ctgntactcc actgncaacc ttntccattg ggctcngtgc cctgtgtngg gtcattggacc 480
 cantccanaa ntatgaatac tgtaccatgc tcttaaccag gaggacctaa ggatccttag 540
 ncccntgagn nanacaccag gnttcaaagg ccgttttggn aagccaaatt tgnttnggnc 600
 cgaattnggg ccaaacangg tt 622

<210> 225
 <211> 619
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(619)
 <223> n = A,T,C or G

<400> 225
 acgcggggag ttccgccatg gcttccttgg aagtcagtcg tagtcctcgc aggtctcggc 60
 gggagctgga agtgcgagc ccacgacaga acaaatattc ggtgctttta cctacctaca 120
 acgagcgca gaacctgccg ctcatcgtgt ggctgctggt gaaaagcttc tccgagagtg 180

gaatcaacta	tgaaattata	atcatagatg	atggaagccc	agatggaaca	agggatgttg	240
ctgaacagtt	ggagaagatc	tatgggtcag	acagaattct	tctaagacca	cgagagaaaa	300
agttgggact	aggaactgca	tatattcatg	gaatgaaaca	tgccacagga	aactacatca	360
ttattatgga	tgctgatctc	tcacaccatc	caaaatttat	tcctgaattt	attagcccg	420
ggggccaatt	ttttaactca	natcttgctg	agaccaggag	catctgattt	aacaggaagt	480
ttcagattat	acccgaaaaa	gaagttctag	agaaattaat	agaaaaatgt	ggttctaaag	540
gctacgtctt	ncaaatggag	atgattggtc	nggcaagaca	gttgaatatt	ctattggcga	600
ggttccatat	canttgngg					619

<210> 226

<211> 277

<212> DNA

<213> Homo sapiens

<400> 226

acgcggggcc	cctcatTTac	ataaatatta	tactagcatt	taccatctca	cttctaggaa	60
tactagtata	tcgctcacac	ctcatatcct	ccctctatg	cctagaagga	ataatactat	120
cgctgttcat	tatagctact	ctcataaccc	tcaacaccca	ctccctctta	gccaatattg	180
tgcttattgc	catactagtc	tttgccgcct	gcgaagcagc	ggggggccta	gccctactag	240
tctcaatctc	caacacatat	ggcctagact	acgtacc			277

<210> 227

<211> 328

<212> DNA

<213> Homo sapiens

<400> 227

ggtacatatt	tttgccaatg	ctatacagca	aaaatgaaaa	acttacagaa	aggtaaacaa	60
aattgagtcc	acttttttaa	tttcacaagc	tgcttttaaac	tatagaacca	ccagatatct	120
gtaaaaataag	caaaactggg	aagtgtgttt	ttttaattga	gggaaggagg	gccagaggag	180
ttggtgcaga	agcgcttcgg	gtgaattcat	accagagcca	ccgggtgtga	ctcggctacc	240
tctcccaatt	accacagggg	ggtcttaaaa	ttgaatttca	gtttcagcag	atactccaga	300
tttacctgag	caatatcata	gacaatgt				328

<210> 228

<211> 609

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(609)

<223> n = A,T,C or G

<400> 228

acgcgggagt	tcaagcagat	gtatggctaa	ccggaaacag	gtgggtcacc	tcctgcaaga	60
agtggggcct	cgagctgtca	gtcatcatgg	tgctatcctc	tgaacccctc	agctgccact	120
gcaacagtgg	gcttaagggt	gtctgagcag	gagaggaaaag	ataagctctt	cgtggtgccc	180
acgatgctca	ggtttggtaa	ccggggagtg	ttcccagggtg	gccttagaaa	gcaaagcttg	240
taactggcaa	gggatgatgt	cagattcagc	ccaaggttcc	tcctctccta	ccaagcagga	300
ggccaggaac	ttctttggac	ttggaagggtg	tgccggggact	ggccgaggcc	cctgcaccct	360
gcgcacagg	actgcttcat	cgtcttggct	gagaaaggga	aaagacacac	aagtcgcgtg	420
ggttggagaa	gccagancca	ttccaacctcc	cttccccaac	atctctcana	gatgtgaaac	480


```

cagatctcat ggcaacnaag cccntngcaa gaagctcaag gaanctaagg aaaatggacg      540
ttttcagana atggttgtag ttcattgggtt ttncctactg ccgggtcctt tcttangacc      600
cgcanaant                                     609

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```

<210> 229
<211> 610
<212> DNA
<213> Homo sapiens

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```

<220>
<221> misc_feature
<222> (1)...(610)
<223> n = A,T,C or G

```

```

<400> 229
ggtacttttt tttttttttt tttttttttt gcagactaaa aatttttattg ctcttttaaag      60
ccttaggccg tatgacaaaa tgaagagact gaaatgacag cggggaggaa gaaacagaag      120
aaagataaga atgaggtggt caggttgagg gaattaagcg aatattctct tccaggtgga      180
gtcctcacac tgggtctcatg cccatgatga gttgcacacc aaacacaggc tgctgacttc      240
ctcctgcac tagtcagtga acttgcagac atagggtaac ctacattac agttataatc      300
ttccacctc agaaatgctg tgcttctcga caggctcgca cagtggccgg ggcttganat      360
ggtggaggga tttctctccc atgcaaagta attcatcaca tcaactgntac tccactccca      420
accttctcca ttgggctcgg tgccctgtgt ggggtcatgg acccaatcca acgtatgant      480
actggtacca atgctnttac cagggaggac acnaaaggat cccttaccoc ctgagcacag      540
accnagggtt tcaaanggcc gttttggcag gccaaactgn atntgnccag aatttgngna      600
caaaacaagg                                     610

```

```

<210> 230
<211> 346
<212> DNA
<213> Homo sapiens

```

```

<400> 230
ggtcggccga ggtaccatgc actgagtgc tgtggggatc atgttggttat aatgaacaca      60
agacacattg cattttctgg aaacaaatgg gaacaaaaaag tatactcttc gcatactggc      120
taccaggtg gatttagaca agtaacagct gctcagcttc acctgagggga tccagtggca      180
attgtaaaac tagctattta tggcatgctg ccaaaaaaacc ttcacagaag aacaatgatg      240
gaaagggttc atctttttcc agatgagtat attccagaag atattcttaa gaatttagta      300
gaggagcttc ctcaaccacg aaaaatacct aaacgtctag atgagt                                     346

```

```

<210> 231
<211> 601
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(601)
<223> n = A,T,C or G

```

```

<400> 231
ggtacgcggg gagagcacat ccggtggttag aagcgctggt aggccttggg gaggcggggt      60
aggaagagtg gagactgctg cacggactct ggaacatga acatatttga tcgaaagatc      120

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WO 00/12702

PCT/US99/19424

aactttgatg	cgtttttaa	attttctcat	ataaccccg	caacgcagca	gcacctgaag	180
aaggctcatg	caagttttgc	cctttgtatg	tttgtggcgg	ctgcaggggc	ctatgtccat	240
atgggtcactc	atttcattca	ggctggcctg	ctgtctgctt	tgggctccct	gatattgatg	300
atttggtctga	tggcaacacc	tcatagccat	gaaactgaac	agaaaagact	gggacttctt	360
gctggatttg	cattccttac	aggagtggc	ctgggcccctg	cctggagttt	tgnattgctg	420
tcaaccccc	atccttccac	tgctttcatg	ggcccgcgaat	gatctttacc	tgcttaacct	480
taatgcactc	tatccaagcg	cgtactcct	tttctgggag	gatcttgatg	tcagcctgaa	540
cttggtgcttt	gcttcctggg	gaatgtttct	ttggatccat	tggctttcca	gcnaactttt	600
t						601

<210> 232

<211> 390

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(390)

<223> n = A,T,C or G

<400> 232

actttttttt	ttttttttt	ttttttttt	ttggttttta	tgttttatttc	cccaagacag	60
cctagcctgc	actctacttg	gataaaat	acaagctagt	tttctgctgc	ttctagtttt	120
aaactttaac	catgtttctg	atgacaagga	atgctgcaaa	aatactctag	ttcaacaaag	180
agttatgatc	acaaaataat	ttttatccat	tctacagtgt	ttcanaatta	ccagttgatt	240
tttaaacaca	aagtagatat	agatgcta	ggtggcta	ctggatgtt	tcttatagca	300
aactgttggt	catgcaacac	ttgtgctcaa	aggggaaggc	acaggatttc	ctacaatgag	360
ccaccttata	aagagttctt	tttgnacctn				390

<210> 233

<211> 603

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(603)

<223> n = A,T,C or G

<400> 233

cgaggtaacg	gggggaagag	tgagggttcc	aacttttctg	cttatctggg	aggtgttggg	60
cgcggaacat	cgagatgtca	gagaaaaagc	agccggtaga	cttaggtctg	ttagaggag	120
acgacgagtt	tgaagagttc	cctgccgaag	actgggctgg	cttagatgaa	gatgaagatg	180
cacatgtctg	ggaggataat	tgggatgatg	acaatgtaga	ggatgacttc	tctaatacgt	240
tacgagctga	actagagaaa	catggttata	agatggagac	ttcatagcat	ccagaagaag	300
tggtgaagta	acctaaactt	gacctgctta	atacattcta	gggcagagaa	cccaggatgg	360
gacactaaaa	aaatgtgttt	atttcattat	ctgcttggat	ttatttgtgt	ttttgtaaca	420
caaaaaataa	atggtttgat	ataagaaaaa	annnnnnnna	aaaaaaaagt	ntggccngg	480
cggccgttca	aanggccaat	tccaccact	ggcgccgta	ctaanggacc	aacttggnc	540
aacttgggga	atcanggcaa	actggttctt	ggngaaatgg	nttcccttcc	aattccccaa	600
atn						603

<210> 234

<211> 616
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(616)
 <223> n = A,T,C or G

<400> 234
 cgaggtacct tc ttgcgat caaaccagat ggggtccagc ggggtcttgt gggagagatt 60
 atcaagcggt ttgagcagaa aggattccgc cttgtttggc tgaaattcat gcaagcttcc 120
 gaagatcttc tcaaggaaca ctacgttgac ctgaaggacc gtccattctt tgccggcctg 180
 gtgaaatata tgcactcagg gccggtagtt gccatggtct gggaggggct gaatgtggtg 240
 aagacgggcc gagtcatgct cggggagacc aaccctgcag actccaagcc tgggaccatc 300
 cgtggagact tctgcataca agttggcagg aacattatac atggcagtga ttctgtggag 360
 agtgcagaga aggagatcgg cttgtggttt caccctgagg aactggtaga ttacacgaac 420
 tgtgtctana actggatcta tgaatgacag gaaggcagac ccattgnttt tcacatncat 480
 ttcccttctt tccattgggc aaaggaccag ctttnggaaa tctantnttt accnggacct 540
 tattcttaat ttgganggaa actnttggac tttgangtnt tcctntacct ngcccgggng 600
 gccgtttaaa agggna 616

<210> 235
 <211> 607
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(607)
 <223> n = A,T,C or G

<400> 235
 acgcggggag tgcgttactt acctcgactc ttagcttgctc ggggacggta accgggaccc 60
 ggtgtctgct cctgtgcgct tcgcctccta atccctagcc actatgcgtg agtgcattctc 120
 catccacggt ggccaggctg gtgtccagat tggcaatgcc tgctgggagc tctactgcct 180
 ggaacacggc atccagcccg atggccagat gccaaagtac aagaccattg ggggaggaga 240
 tgactccttc aacaccttct tcagttagac gggcgctggc aagcacgtgc cccgggctgt 300
 gttttagtag ttggaaccca cagtcattga tgaagtctgc actggcacct accgccagct 360
 ctccaccctg agcagctcat cacaggcaag gaagatgctg ccaataacta tgcccgangg 420
 cactacacca ttggcaagga gatcattgac cttgngttgg acccaattcc aaacctggct 480
 gaccatgcac ogggctttan ggnntnttgg gttttcccaa antttggggg ggaactgggt 540
 ttgggttaac ttctgtntna tggnacgntt ttaaataaat ntgggaaaaa tccaactggn 600
 gntttcc 607

<210> 236
 <211> 608
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(608)

<223> n = A,T,C or G

<400> 236

acgcgggcat	gcaacaccac	acccagcctg	aaaccagat	ttttaatatg	aaatcaaagt	60
cttcagacct	tgtagggtgc	ataaaaagca	cgctgaggac	cactagtgtg	caactgccaa	120
tctaaaatat	catagacatt	atatcacttc	aaccacgaaa	aaaaagtatg	tgaggcagaa	180
aatggaagca	accatgccta	atttattgtt	gaatactttt	tccgtatacc	aagagcttcc	240
tttgcactag	catctgaaac	tatatccaga	atgacactgg	ttttcataaa	agtgttgatc	300
ctcacacctc	tttatagtct	tgcacctagc	acagtggagt	gaaacacttt	aaatagcact	360
tgntccttga	gtatatatgg	aaaaaagtga	agtattgata	aagtgtctca	ctaatatgag	420
cagcatctca	ggagtctcca	attcttgaat	taccaggag	tatttttacc	attttcccca	480
ntgnaaggcc	ttttttgaga	nacttaccct	caaataanga	gnnttaagca	tgntcctttt	540
tttttccttt	tttttttgan	aaaagggtct	gctntgtggc	caggttggan	tgccacntg	600
aaaattcn						608

<210> 237

<211> 609

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(609)

<223> n = A,T,C or G

<400> 237

actatttcat	atattgtgtg	agccccacaa	atgtctat	taaaaagagt	atagtccctg	60
gccaggcgcg	gtggctcacg	cctgtaatcc	cagcagtttg	ggaggccgag	gtgggcggat	120
cacctgaggt	ctggagtctg	agaccagcct	gaccaatatg	gtgaaacccc	gtttctacta	180
aaaatacaaaa	attagctggg	catgggtggag	catgcctgta	atcccagcta	ctcggggaggc	240
tgaggcagga	gaatcacttg	aacccgggag	gcgaaggctg	cagtgaagcca	agatcacgcc	300
attgcactcc	agcctgagca	acaagaggga	cactccgtcc	ccaaaaaaaa	aataataaaa	360
aaaataaaaa	ataaaaaata	aaagagtata	gttcccaatg	ggttctacaa	acattcctga	420
tttatactgg	gggaagtgat	gcctaantgg	gaacattaat	cattatgggt	tcgaaaatta	480
aatattttctg	caaacaattc	ctttgcaaat	gctaacttgc	catgagctta	ccccatttga	540
aattgngnct	ttacaaagac	cttggccgga	ccccttangg	ngaattcagn	cactggngggg	600
cgttcctttg						609

<210> 238

<211> 616

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(616)

<223> n = A,T,C or G

<400> 238

acgaggcggt	gcgggaagtc	ctgcacggga	accagcgcaa	gcgccgcaag	ttcctggaga	60
cggtggagtt	gcagatcagc	ttgaagaact	atgatcccca	gaaggacaag	cgcttctcgg	120
gcaccgtcag	gcttaagtcc	actccccgcc	ctaagttctc	tgtgtgtgtc	ctgggggacc	180
agcagcactg	tgacgaggct	aaggccgtgg	atatccccc	catggacatc	gaggcgctga	240

```

aaaaactcaa caagaataaa aaactgggtca agaagctggc caagaagtat gatgcgtttt 300
tgacctcaga gtctctgata aagcagattc cacgaatcct cggcccaggt ttaaataagg 360
caggaaaaagt tcccttcctg ctcacacaca acgaaaacat ggtggccaaa agtggatgag 420
gtgaagtcca caatcaagtt ccaatgaaga aggggtatgt ctggcttgta acttggtggg 480
cacgtgaaga tgacngacga tgacttgngt ataacattna nctgggctgg caacttcttg 540
gggcaatgnt caanaaaact ggcaaaatgt ccgggccttt tttttagagc cccttggnaa 600
accccgangc ntttta 616

```

<210> 239

<211> 607

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(607)

<223> n = A,T,C or G

<400> 239

```

acagtctgtt cgagaacacc ttgggtcatga aagtgacaac ctgctgtttg ttcagatcac 60
aggcaaaaaa ccaaaactttg aagtgggttc ttctaggcag cttaagcttt ccatcaccaa 120
gaagtcttct ccttcagtga aacctgctgt ggaccctgct gctgccaagc tgtggaccct 180
ctcagccaac gatatggagg acgacagcat ggatctcatt gactcagatg agctgctgga 240
tccagaagat ttgaagaagc cagatccagc ttccctgcgg gctgcttctt gtggggaaaag 300
ggaaaaagag gaaggcctgt aagaactgca cctgtggcct tgccgaagaa ctggaaaaag 360
agaagtcaag ggaacagatg aacttccaac ccaagtcaac ttgtggaaac tgctcctggg 420
cgatgccttt cgttgtgcca ctggccctac cttgggatgc cagcntnaaa ctggggaaaa 480
gngcttctaa tgatancatc tttattgaag cctaagaagg ttctgaattg ggacccattt 540
gttcttcaac caattctggn cttaaatcca cttgggggtt cttccacctc cttggatttg 600
ncacett 607

```

<210> 240

<211> 615

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(615)

<223> n = A,T,C or G

<400> 240

```

ggtacgcggg gcttttcaca agatggcgcc gaaagcgaag aaggaagctc ctgccccctc 60
taaagctgaa gccaaagcga aggttttaaa ggccaagaag gcagtgttga aaggtgtcca 120
cagccacaaa aagaagaaga tccgcacgtc acccaccttc cggcggccga agacactgcg 180
actccggaga cagcccaaat atcctcggaa gagcgctccc aggagaaaca agcttgacca 240
ctatgctatc atcaagtttc cgctgaccac tgagtctgcc atgaagaaga tagaagacaa 300
caacacactt gtgttcattg tggatgttaa agccaacaag caccagatta aacaggctgt 360
gaagaactgt atgacattga tgtggccaag gtcaacaccc tgattcggcc tgatggagag 420
aagaaggcat atgttcgact ggctcctgat tacnatgctt tggatgttgc caccaaaatt 480
gggatcattt aactgagtc acttgctaaa tctgaatata tatatatata tatatctttt 540
cncccaaaaa aaaaaaaaaa aaaaaagtn tncggcgcg ccgttttaaa ggggaattccc 600
cacttggggg cgttt 615

```

<210> 241
 <211> 365
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(365)
 <223> n = A,T,C or G

<400> 241
 acgggggggt cgctttgctg ttctgtgatat gagacagaca gttgcggtgg gtgtcatcaa 60
 agcagtggac aagaaggctg ctggagctgg caaggtcacc aagtctgccc agaaagctca 120
 gaaggctaaa tgaatattat ccctaataacc tgccacccca ctcttaatca gtggtggaag 180
 aacggtctca gaactgtttg tttcaatttg ccatttaagt ttagtagtaa aagactgggt 240
 aatgataaca atgcatcgta aaaccttcag aaggaaagga gaatgttttg tggaccactt 300
 tggttttctt ttttgcgtgt ggcaagtttt aaagttatta agttttttaa atcaagtacc 360
 tnggn 365

<210> 242
 <211> 625
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(625)
 <223> n = A,T,C or G

<400> 242
 natngganng nttttccctt aacgtgggcc ncggccgagg nacttttttt tttttttttt 60
 tttttttttt gcaggcagct atttaattan gntcttaana catttanaac nccaatttgn 120
 gaanataaat tccattcgctc anaacaaacn cagatcgcan gtagccctgg anctgangaa 180
 taactttgat ttttggnaaa atttgngagt ccncagcttt ctgatcaatc ttgcgctgct 240
 ccnaatctc atatttctct ttttctgggg ccaaaatctt accttctctg ngctctgggt 300
 ttgcgaactt cttcttcttg aaagaagcct cagtaaaaaat ggtttgggaa ttttacatta 360
 ctgatatcca atttnggtga aatggcaatg accaatttct nggggggtct tcgtaaaaga 420
 actccantga nggnccaaaq gtccagtcac aagtataggc nctnaccact gnttcaggaa 480
 accacctttt gncctggggg gtccatgagg atgaccaaataa ggncccgggg naagctgggt 540
 ccantttttt acggcctacc gaagggtttt tgccnnggta aaagttttag ggccattttc 600
 ngggnaaatc taggcttttt gaaat 625

<210> 243
 <211> 639
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(639)
 <223> n = A,T,C or G

<400> 243

nncnaattcc	ncntaaccn	ggnccccgc	caagnacccc	ggcncctttg	gatgtatnga	60
aatnaacnta	ttaatgggga	cntattggag	aaggaaatnc	ctagacctac	aacttttnagc	120
naatagcngt	gatgttttag	gaactgaaat	gtcacactta	aagtcttnag	cccagctact	180
tccctatttt	tgtggggaga	aaanggccng	attagaactg	ttctgggtgt	gtttggcggg	240
aggggaataa	tttttgttca	gtcctttctta	gtgaccaaac	tttaattttt	aagaataata	300
tattgactta	ctgaactgaa	gcattctgag	ttgaaaggag	ctccncagga	ntggagttct	360
gtgttgctca	catgttnaaa	ncttgcctac	cttnatagcn	caaggaatac	ctatcttcca	420
natnccgcca	ttttcatctc	ttaaattgnag	tccaaagtat	gacttgagaa	agttgctctn	480
ggattctggg	gtcttaaaac	tngggattct	gggattntgg	ggtccnaaag	ttnaccttgn	540
aaagtgcct	gggnttttan	aaatnncctg	nattctg_	ttttaaaaaa	ttttgaaaaa	600
acccncccn	ncttgaaagg	gaccttaaaa	attaacctn			639

<210> 244

<211> 614

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(614)

<223> n = A,T,C or G

<400> 244

tcgagccgnc	ggcccgggcc	aggtactttt	tttttttttt	tttttttttt	gaaaatggag	60
tcttgctctg	ntgccaaact	ggantgcaat	ggtgcganct	gggctcactg	naatctccac	120
ctnccgggtt	caagcgattc	tcttgcttca	cctccgagta	actgggacta	caggtgcgcg	180
ccaccaagcc	cagctcattt	ttgnattttt	agtanaaatg	gggtttcacg	atgttggtta	240
ngatggntct	gatctctggt	caaagtcttt	tctgnaaata	tccttggtta	aaaaacaatt	300
ttagactgta	gctgttgcaa	atgctttaag	gaagaaacna	aacaactgca	gtcttcctga	360
aatgaaaaaa	ctccccaggg	ctgctattna	aaacaacccc	accagcactt	caatcatgat	420
gccnacagtg	gcccactgaa	aaancnggaa	aagttcnaat	cccaaactgg	gatgctcttg	480
actntggaat	tntgnnggcn	ntncccnant	ttnanacaaa	acngnctngg	nccctntttt	540
ttgggggaat	ttgggaanaa	aaaaacttgn	gngttcttgn	ggttcctntg	ttccccaaaa	600
nactgggggn	nggg					614

<210> 245

<211> 620

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(620)

<223> n = A,T,C or G

<400> 245

gccgtgggtc	cgggccgagg	tccatttgcc	tcccggcctc	aagccgattc	tccctgcttca	60
gcctccaag	tagctgggga	ttacaggcac	ctgccaccat	gcccggctaa	tttttgnaat	120
tttagtagag	acagggtttc	accatgttgc	ccaggctggt	ttcgaactcc	tgacctcagg	180
tgatccaccc	gcctcgccct	ccaaagtgtc	gggattacag	gcttgagccc	ccgcgcccag	240
ccatcaaaat	gctttttatt	tctgcatatg	ttgaataact	tttacaattt	aaaaaaatga	300
tctgntttga	aggcaaaatt	gcaaactctg	aaattaagaa	ggcaaaaatg	taaaggagtc	360

```

aaaactataa atcaagtatt tgggaaagtg aagactggaa gctaatttgc attaaattca    420
caaactttta tactctttct ggatatacat tttttttctt taaaaaaciaa ctttngatca    480
gaatagcccc atttagaacc ttttggtatc agncaatatt tttaaatagt tnaaccnggc    540
ctaagctnaa agnggcttga tntgagtaaa cttttcaact ggcttgaacc ctnaaccttt    600
taaaatgacc ttccgagntt

```

```

<210> 246
<211> 595
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(595)
<223> n = A,T,C or G

```

```

<400> 246
acttattctt caggggttac tgagtcggca cctatgacag ctaagagagc tttcttaaag    60
actgcctcag tgtcttcttg gcttttggca ccttcactcc actctgccc ggaaatccac    120
aatggcagac aaacctgggg tttcaggtgc acaaagactt cttcaaaaag catggctatg    180
tcagggctct ttgactcgat cagcacctgc agcttcagct gccacattgt cccagagtct    240
ctaacaatt caagttccag ctactgncac ttccagagct tcttcaggaa gttataacac    300
agcaacgaaa cactcaactg cttgtattgg cattctgaca gaagcttcaa gttcatgtgc    360
cttctgaat acagtcattg tctttncaac ctcttctctt aaggaccac tatttgactt    420
cttaataaat ctttccagcc aaaggngatg aacactttca catgggcctt gtggcaaaaag    480
cttnatggct ttttatcncg gacagacctt tctcttcggg cgacctcaat ggtttggtt    540
ggtcgtggag ctggtntttg gctnggactc aacttnaatt ttgcttgccc naaac        595

```

```

<210> 247
<211> 364
<212> DNA
<213> Homo sapiens

```

```

<400> 247
gggtacacta gaaagtcttt tacaaaataa tcatcttaga tcaacagaag accaatcttc    60
aatgtcgtcc tgcaagatgg gttactttta catctcctcc tgttttctcc aatgttctcc    120
tttagtatgg ctggtaatg ttttggtgat tgccaccccc tcgagatgcc ttgccataag    180
tgctctgttg gccactgtag tctgcatac cctgtccata tccatagtcc ccatagtatt    240
accagttata atcatatccg ccatagccac tatagttttg atcaccacca taggcactat    300
tgtaatttcc atatccttga tcataatagt tattaaatcc ttggttccag ttttggccct    360
gacc

```

```

<210> 248
<211> 591
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(591)
<223> n = A,T,C or G

```

```

<400> 248

```



```

ggtnccagata tcttcaaagg aggaagaaga aagggaaacc agatgggtgga cctgaatatg      60
ncccttancc aganctaata aaccactca gccagaatag aagaagctgg aatagattcc      120
ccaacctggg ttgccagttc atcttttgac tctattaaaa tcttcaatag ttggtattct      180
gnaatttcac tctcatgant gcnactgngg cttaactaat attgcaatgn ggcttgaatg      240
taagtagcat cctttgatgc ttctttgaaa cttgnatgaa ttgggtatg aacagattgc      300
ctgctttccc ttaataaaca cttaaaatta tttggaccag tcagcacaac atgcctnngt      360
tgnattaaag cnnnggatatg ctggatttta taaaattggc caaattagag aaatntagtc      420
ccatggaaat atattttcttg taaaaaagt cttgaatctt tttggtcaag ataatgccac      480
tcttaagaat atcttcncac tnttgangga ttaaataatcg gcantggaaa agccttaaaa      540
atgggggtcna cttgccttgn gcctaaaccg accctgaaat gggattttccc n      591

```

<210> 249

<211> 332

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(332)

<223> n = A,T,C or G

<400> 249

```

acttccgag agggctcggtt tcccgteccc gagagcaagt ttatttacca aatgttggag      60
taataaagaa aggcagaaca aaatgagctg ggctttggaa gaatggaaag aaagggtgc      120
ctcaagagct cttcagaaaa ttcaagaact tgaaaggaca gcttgacaaa ctgaagaagg      180
aaaagcagca aaggcagttt cagctttgac agtctcgagg cttgcgcttg cagaaacnaa      240
aacagaaagg ttgaaaatga aaaaaccagc ggtaccttgg nccgggacca cgcttaaggc      300
gaaattccaa cacacttggc cggccggtac ta      332

```

<210> 250

<211> 626

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(626)

<223> n = A,T,C or G

<400> 250

```

ggtactatta gccatgggtca accccaccgt gttcttcgac attgccgtcg accggcgaaag      60
ccctttggcc cgcgtcttcc tttgaactgg ttgcagacaa ggggtcccaa ganagcagaa      120
aattttcgtg ctctgagcac tggagaaaaa ggatttggtt ataagggttc ctgctttcac      180
agaattattc caggggttat gtgtcaaggt ggtgacttca cacgccataa tggcactggg      240
ggcaaagtcc atctatgggg aagaaatttg aagatgaaga acttcatcct aaagcatacg      300
ggtcctggca tcttgtccat ggcaaagtct ggacccaaca caaatgggtc ccaatttttc      360
atctgcactg gccaaagact antggttgga tggcaaanca tgtngtgntt ggccaaagtg      420
aaagaaggca tgaatattgt ggaaggccat ggaacgcttt tgggtncnag gaatggcaag      480
aaccnccagg aagaatcacc cnttnttgac tggggacaa tcnaataagt tgacttgggg      540
nttaanttaa cccccanca attccttttg gaactcagga aacacccttc anccanttn      600
tttcaanttc caaaannttg ggccn      626

```

<210> 251

<211> 603
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(603)
 <223> n = A,T,C or G

<400> 251
 actttttttt tttttttttt tttttttttt aacagaagaa cttttngttt ctttattttc 60
 aatatngtgc ttattaatat ttttcttatt ttataatgca attacaacaa tttaggagac 120
 aaaacantat aaacaaaaga atgttaaata gtttttttta aaaaatagct tgttgcttgc 180
 aagaaagtcc atataatctt attccccccc aaatataatt ttatactttg cactaaacca 240
 aaatagctta tggaaaatta ggtattaaat agctaaacac agaaaaccta cagctataaa 300
 taacataaaa tacagtttaa ctttaaatgng atgcttaaac aaagcaaact atgatgcant 360
 atgaatcaac ttcattaatt ggacaagtcc agtgaggcnc aaattagata agcnctaaac 420
 cctcatgatg ggcaagtga accttcaccc cagcaagggt ctttcnggtc ttggctatgc 480
 caattccttc canaaaagnc ccagttttac angtctggct tttccggggg gaacccccca 540
 tttnttttnc ccaagttggt tnggatttgg ccccccannaa attttttttg gngnaaaaaan 600
 aan 603

<210> 252
 <211> 500
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(500)
 <223> n = A,T,C or G

<400> 252
 actttatttg ttttttttgt tttgttttgg tttttttttt ggcttgactc aggattttaa 60
 aactggaacg gtgaaggtga cagcagtcgg ttggagcgag catcccccaa agttcacaat 120
 gtggccgagg actttgattg cacattgttg tttttttaat agtcattcca aatatgagat 180
 gcattgttac aggaagtccc ttgccatcct aaaagccacc ccacttctct ctaaggagaa 240
 tggcccagtc ctctcccaag tccacacagg ggaggtgata gcattgcttt cgtgtaaatt 300
 atgtaatgca aaattttttt aatcttcgcc ttaatacttt tttattttgt tttattttga 360
 atgatgagcc ttcgtgcccc cccttcccc ttttttgtcc cccaacttga gatgtatgaa 420
 ngcttttggg ctccctggga agtgggtgga ngcagccagg gcttacctgt accttggccg 480
 cgaacaccta aggccaanntt 500

<210> 253
 <211> 634
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(634)
 <223> n = A,T,C or G

```

<400> 253
tcgagcggcc ngcccgggca ggtactatta gccatggtca aacccccaccc gtgttcttcg      60
acattgcccg tgcagcggcg acccttgggc ccgcgtctcc tttgagctgt ttgcagacaa      120
gggtcccaaag acagcagaaa attttcgtgc tctgagcact ggagagaaag gatttggtta      180
taagggttcc tgctttcaca gaattattcc aggggttatg tgtcaggggt ggtgacttca      240
cacgccataa tggcactggg ggcaagtcca tctatgggga gaaatttgaa gatgagaact      300
tcacccataa gcatacgggt cctggcatct tgtccatggc aaatgctgga cccaacacaa      360
atggttccca gtttttcac tgcactgcca agactgantg gttggatggc aaacatgtgg      420
tgtttgggcaa antgaaagaa ngcatgaata ttgtggaagc catgganccc tttnggtcca      480
ggaatggcag aacnncagg aanacaccct tgntgactgt ggcaactcga ataaattgac      540
ttgggggttat cttaaccncc caacattcct ttggacttag gaancanccc ttcancecnt      600
tggttcaant tcccaaaaat ttgggctncc tnnng                                     634

```

```

<210> 254
<211> 602
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(602)
<223> n = A,T,C or G

```

```

<400> 254
nctttttttt tttttttttt ttttttaaat taattaatta aaaaataggt ggnctactgg      60
tggtccttaa gctggaantg cagtgggcac aatcatggnt cactgnagtc tnaacctncc      120
agggtcaagt gatcctccta cctcacctcc antagctggg attacaggca tatgcgacca      180
tgcccagcta attttttatt ttttgtaaaa acgggggtctc actatgtcgc ccangctggn      240
cttgaactcc tgaactcaag tgacccttcc gncnacctn caaagtgcta ggcttacagg      300
tgtgaaccac catgcctggc ctaaaaaatt tatttttaaaa aagtaattta tctcttacag      360
ttgtggaggg tgagaaatcc aangncaant ggcncatttg gtgaaaacct tnttgctggg      420
ggggactctg tgaaatnccc aantggcnca tgcatnacac antgangggg cttacattcc      480
aacatgctat ctcttttaag ttttaaagta cnggccnaaa tntgaacntg aatgacttna      540
aatccacnca ttccnctttt ggacnaaaaa cntggggcaa ttgggatctt ggcnttttna      600
aa                                                                                   602

```

```

<210> 255
<211> 614
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(614)
<223> n = A,T,C or G

```

```

<400> 255
cgaggtacag gtaagccctg gctgcctcca cccactccca gggagaccaa aagccttcat      60
acatctcaag ttggggggaca aaaaaggggg aagggggggc acgaaggctc atcattcaaa      120
ataaaacaaa ataaaaaagt attaaaggcg agattaaaaa aattttgcat tacataattt      180
acacgaaagc aatgctatca cctcccctgt gtggacttgg gagaggactg gaccattctc      240
cttagagaga agtgggggtg cttttaggat ggcaagggac ttcctgtaac aatgcatctc      300
atatttgga tgaactattaa aaaaacaaca atgtgcaatc aaagtccctg gccacattgt      360

```

```

gaactttggg ggatgctcgc tccaaccgca ctgctgtcac cttcaccggt ccagttttta 420
aatcctgagt caagccaaaa aaaaaaaacc anaccaaact nanaaaacaa ttaagccatg 480
ccaatctcat ctggtttctg cncaagtang gttgncaaaa aagggttacc ncactaantc 540
ntagccccta aaccnttgcg ggggncantg angggccgan tttganactc cggntggtga 600
nccanttggg ggag 614

```

```

<210> 256
<211> 308
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(308)
<223> n = A,T,C or G

```

```

<400> 256
nntccagca gtgggtcatt cgncaacgaa agtcntaccg tagaaaagat ggcgtgtttc 60
tttattttga agataatgca ggagtcatag tgaacaataa aggcgagatg aaagggtctg 120
ccattacagg accagtagca agggaatgtg cagacttgtg gccccggatt gcatccaatg 180
ctggcagcat tgcattgatt tccagtatat ttgtaaaaaa taaaaaaaaa ctaaacccaa 240
aaaaaaaaat nnnannnaac annnnanaaa aannnnnaaaa aaaaaaaagta cctnggccgn 300
gaccacgc 308

```

```

<210> 257
<211> 602
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(602)
<223> n = A,T,C or G

```

```

<400> 257
gcgtggctgc nggccgaggt acgcggggga gacaaaccat accatatccc accagagagt 60
cgcagacact atgctgcctc catggccctg cccagtgtat cttggatgct gctttcctgc 120
ctcatgctgc tgtctcaggt tcaagggtgaa gaaccccaga gggaactgcc ctctgcacgg 180
atccgctgtc ccaaaggctc caaggcctat ggctcccact gctatgcctt gtttttgtca 240
ccaaaatcct ggacagatgc agatctggcc tgccagaagc ggccctctgg aaacctggtg 300
tctgtgctca ntggggctga gggatccttc gtgtcctccc tggatgaagag cattggtaac 360
agctactcat acgtctggat tgggctccat gacccacacac agggcaccga acccaatgga 420
aaangntggg antggaataa cantgatgtg atgaattact ttgcatggga gagaaatcct 480
tcancatttt naacccggc cctgccaac ctntcaaaaa cncacatttt taaggggaaa 540
attttactgg atggganggt acccttttnt ggaagtactg cttttcngga nggaagtacc 600
cc 602

```

```

<210> 258
<211> 600
<212> DNA
<213> Homo sapiens

```

```

<220>

```

<221> misc_feature
 <222> (1)...(600)
 <223> n = A,T,C or G

<400> 258
 ggtgntgtg ncttatntgt agcggcgcg ntggttctga aatcgccctt agcggcgccg 60
 cagtentatt atgtgnatgt ccctaccacn aaaatncaga ttaattggna tgctcattac 120
 ccacgtgaac gccaaagccc ttcgaagtag tgctgccctg cactnaatca agaagttgca 180
 ttaaaattag aaccaaattc agagtcactg gaactttctt ttaccatgcc ccanattcag 240
 gatcagacac ctagtccctc cgatggaaag cactagacaa agttcacctg agcctaatag 300
 tcccagtgaa tatttggttt atggggatag gtgatattgn caatgaattc aagttggaat 360
 tgganagaaa actttttgct naagacncng aagcnaagaa ~ccattttct actnaaggca 420
 cagatttaga cttggagatg gtagcttctt atatccaatg gatgatgctt tcagtccgtn 480
 cnttgatcag tgnacnttn gaaagcagtt cccaagnctt gnaacccagt cctaagccaa 540
 gtccggttcn gcgattaatc cgactatgta tgcccttcat ngcccctgtn ataaacnggn 600

<210> 259
 <211> 600
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(600)
 <223> n = A,T,C or G

<400> 259
 gccgaggtac atgggaaagg gagtatggng agctattttcc tttttaaagg atgaagacct 60
 tcataaattg gccctcggga ttctgggtgat tcccgcgcgc aagcgcaaat gctccagtgn 120
 gttatgaaaa tgnttgntaa tctgctctgg ttcttcactg gattcaagan tcgggaggnc 180
 ttctcgaatc ttttgataaa nctggtttaa aacctgaatt gntaccgcga tcattttcct 240
 tttcataaaa atagatatat ctgntcagaa tttctatnaa aagctgcact tgtaganang 300
 ggtccatgca ctgatttgct attttttaaag ctttttttan gcactccatt accctnttgc 360
 cttcgtgaaa cttcttccca tttttgncn gggtctggcn gaccngaaga aatgtgcccc 420
 agtgcttaca agttnggctt gacaagggtc nttaaaantt tggatgtacc aaggggcccc 480
 tgggtcctca aaggtcatga atctttttac tggaaccctt atccttttnaa aaggccatgg 540
 tcaagggaat gnncttcttg gctttgaaac ccggattaan tttttncaa aaaagccngn 600

<210> 260
 <211> 593
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(593)
 <223> n = A,T,C or G

<400> 260
 acgcgggaac tccatcctca ccaccacac caccctggag cactctgatt gtgccttcat 60
 ggtagacaat gaggccatct atgacatctg tcgtagaaac ctcgatatcg agcgcccaac 120
 ctacactaac cttaaccgcc ttattagcca gattgtgtcc tccatcactg cttccctgag 180
 atttgatgga gccctgaatg ttgacctgac agaattccag accaacctgg tgccttacc 240

```

ccgcatccac  ttcctctggc  cacatatgcc  cctgtcatct  ctgctgagaa  agcctaccat  300
gaacagctta  ctgtagcaga  gatcaccaat  gcttgctttg  agccagccaa  ccagatgggtg  360
aaatgtgacc  ctgcgccatg  taaatacatg  gcttgctgcc  tggatataccg  tggtgacntg  420
ggtncaaaag  atgtcaatgc  tgccttggca  ccattcaaac  caagcgcaga  ttcaatttgg  480
ggatgggtgcc  cactggcctt  aaggtngnat  naactaccag  cttccactgn  ggnnctgggtg  540
gaaactngcc  aaggnnccct  ggccggaaca  ccctangggg  aattcanncc  act  593

```

```

<210> 261
<211> 343
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(343)
<223> n = A,T,C or G

```

```

<400> 261
cctacctctc  ttncactgc  aaatttcttg  gatagaccaa  aagtgaattt  gattatgtgt  60
tggtgaagt  tcttcattct  gactgttgan  gggaggtttt  cctttgaaga  gttttcatcc  120
cagactcagc  tgtcttttca  catggatgaa  ataattcctg  ctaccaacaa  cagagcttca  180
ccaggaagtt  gagttttcaa  gatgccttgt  tgctttgaag  aagggagtga  tgtcaattct  240
cttgntacat  tctcccttta  gcaacctgag  taagagactc  tctgccactg  ggctgcaaaa  300
aaataaatta  cttgaatctc  cccttggccc  angctgaggt  acc  343

```

```

<210> 262
<211> 593
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(593)
<223> n = A,T,C or G

```

```

<400> 262
actttttttt  tttttttttt  ttttttttgt  tttttttttt  tttttttttt  tttttttttt  60
tttttttttt  ttacagngtn  ttttcatttt  tattactcaa  aaaagtttca  tttttttnat  120
ttanctttnt  gactntgggc  ttgggccttn  aacantttca  naacgatttt  ntgctcctcg  180
anaaggaaag  cnccttgat  cctgncacna  acncttttag  cncacatgga  accnccatag  240
gccctgntga  catgtttctt  tgtttnggac  aatntcataa  aaacttttagg  nnttacagca  300
cnaacccctn  naagtntgcc  tgggncaca  ccanatgcaa  attttggggc  tttcccaacc  360
ttnttggnat  aaaggtaaac  aattttttta  ccaggggggt  cgggacaacc  tanttttgtt  420
aaaggctgta  ttgtaggaaa  acctacctcg  ggatgtcaaa  cccttnacca  ttttgagggg  480
ctggaaanaa  ngttcccgga  aancctcggt  tancttnggc  cggaaccccc  taangggnga  540
attccnacn  cttgggggcn  gtantaaggg  ganccaantt  gggccaaant  tgg  593

```

```

<210> 263
<211> 591
<212> DNA
<213> Homo sapiens

```

```

<220>

```

<221> misc_feature
 <222> (1)...(591)
 <223> n = A,T,C or G

<400> 263
 accaagagtt tgctcctggc tgctttgatg tcagtgtctgc tactccacct ctgcggcgaa 60
 tcagaagtaa gcaactttga ctgccgtctt ggatacacag accgtattct tcatcctaaa 120
 ttatttggg gcttcacacg gcagctggcc aatgaaggct gtgacatcaa tgctatcatc 180
 ttccacaaag aaaaagttgt ctgtgtgctgc aaatccaaaa cagacttggg tgaaatatat 240
 tgtgcgtctc ctacagtaaaa aagtcaagaa catgtaaaaa ctgtggcttt tctggaatgg 300
 aattggacat agcccaagaa cagaaagaac cttgtctgggg ttggagggtt cacttgcaca 360
 tcatggaggg tttaatgctt atctaatttg tgccctactg gacttgncaa ttaatgaagt 420
 gatcatattg catcataagt ttgctttggg taancttaca ttaaagttaa ctggatttga 480
 agggaattat actgtagggt ctggggtaac tatttaatac taattttcat aacnattttg 540
 gttaatncca agttnaaatt tatttggggg gaanaaaatt tttggccttc t 591

<210> 264
 <211> 595
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(595)
 <223> n = A,T,C or G

<400> 264
 accaagagtt tgctcctggc tgctttgatg tcagtgtctgc tactccacct ctgcggcgaa 60
 tcagaagtaa gcaactttga ctgccgtctt ggatacacag accgtattct tcatcctaaa 120
 ttatttggg gcttcacacg gcagctggcc aatgaaggct gtgacatcaa tgctatcatc 180
 ttccacaaag aaaaagttgt ctgtgtgctgc aaatccaaaa cagacttggg tgaaatatat 240
 tgtgcgtctc ctacagtaaaa aagtcaagaa catgtaaaaa ctgtggcttt tctggaatgg 300
 aattggacat agcccaagaa cagaaagaac cttgtctgggg ttggagggtt cacttgcaca 360
 tcatggaggg gtttagtgct tatctaattt gtgcctcact ggacttgtcc aattaatgaa 420
 gttgattcat attgcatcat agtttgcttt ggtaagcat cacattaaag ttaactgga 480
 ttttatggta tttatagctg nanggtttct ggggttanc ttttaatact aaattttcat 540
 aagctttttg ggtaangcc aagnttaaaa tttttttggg ggggaaaaaa atttt 595

<210> 265
 <211> 592
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(592)
 <223> n = A,T,C or G

<400> 265
 ggtacttttt tttttttttt tttttttttt ttgaaaatta tactttttatt tgagtcacca 60
 ggagaaagat tcaacttggt ttcaagtcaa atgttcanaa tcataacagg ccanaaagg 120
 ttgatcccgga gcacaagccc acgagggagg ggacccaaac agaccaaaat gagacaacaa 180
 ccccatataa aaagatgaac tggcggcttc acacactcac acacatacac atacacacgg 240

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```
<210> 266
<211> 594
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> misc_feature
<222> (1)...(594)
<223> n = A,T,C or G
```

```
<210> 267
<211> 598
<212> DNA
<213> Homo sapiens
```

```
<220>  
<221> misc_feature  
<222> (1)...(598)  
<223> n = A,T,C or G
```

<210> 268
<211> 590

<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(590)
<223> n = A,T,C or G

<400> 268
ggacatatta tcaataggct ataagatgta acaacgaaat gatgacatct ggagaagaaa 60
catctttttcc ttataaaaaat gtgtttttcaa gctgtttgtt taagaagcaa aagatagttc 120
tgcaaattca aagatacagt atcccttcaa aacaaatagg agttcaggga agagaaacat 180
ccttcaaagg acagtgttgt tttgaccggg agatctagag agtgctcaga attagggcct 240
ggcatttgga atcacaggat ttatcatcac agaaacaact gttttaagat tagttccatc 300
actctcatcc tgtatttttta taagaaacac aagagtgcac accagaattg aatataccat 360
atgggattgg agaaagacaa atgtggaaga aatcatagag ctggagacta cttttgtgct 420
ttacaaaact gtgaaggatt gtggtcacct ggaacaggct tncaatctat gtagcactat 480
gtggctcanc cttgggtacc cttggattat atatcaacct gnaacatgng nctgggactt 540
actttcnaaa cnaaatnttc cttntttgaa gaaaatctgg gtttttgnaa 590

<210> 269
<211> 602
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(602)
<223> n = A,T,C or G

<400> 269
acttgaagga agtcgaatca gagatagact ctgaagaaga acttataaat aaaaaaagaa 60
tcatagagaa agttattcat cgactcacac actatgatca tgttctaatt gagctcaccc 120
aggctggatt gaaaggctcc acagagggaa gtgagagcta tgaagaagat ccctacttgg 180
tagttaaccc taactacttg ctogaagatt gagatagtaa aagtaactga ccagagctga 240
ggaactgtgg cacagcacct cgtggcctgg agcctggctg gagctctgct agggacagaa 300
gtgtttctgg aagtgatgct tcaggatttg ttttcagaaa caagaattga gttgatggct 360
ctatgtgtca cattcatcac aggtttcata ccaacacagg cttcagcact tncntttggg 420
ggtggttcct ggtcccntgg aagttggaac caaattaatg gngtagtctc tatacccaat 480
acctttgggt ttcatgtgta anaaaaaggn ccattacttt taanggattg tgctggncct 540
attgngccan taactttttt ttaaattggc cagttacngg ttttaattct taaaannaaa 600
aa 602

<210> 270
<211> 595
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(595)
<223> n = A,T,C or G

```

<400> 270
ggtagcgcggg ggtaggagcc tctctcccta ctgctgctac acaagaccct gagactgacc      60
tgcaggacga aaccatgaag agcctgaccc ttcttgccat cctggccgcc ttagcggtag      120
taactttgtg ttatgaatca catgaaagca tggaaatctta tgaacttaat ccttccatta      180
acaggagaaa tgcaaatacc ttcatatccc ctccagcagag atggagagct aaagtccaag      240
agaggatccg agaacgctct aagcctgtcc acgagctcaa tagggaagcc tgtgatgact      300
acagactttg cgaacgctac gccatggttt atggatacaa tgctgcctat aatcgctact      360
tcaggaagcg ccgaggggacc aaatgagact gaggggaagaa aaaaaatctc tttntttctg      420
gaggctggca cctgattttg tatccccctg tagcagcatt actgaaatac ataggcttat      480
atacaatgct tctttctgga tattctcttg gcttgggtgg accccttttt ccggccccag      540
aattgttaan taatngaann nccntncann aagggnnnaa aggnaaatca ncttt      595

```

```

<210> 271
<211> 592
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(592)
<223> n = A,T,C or G

```

```

<400> 271
ggtagcattga gatcccgccct ctacaaaatc aaaaaattag ccaggcaagg tgggtgcgtgc      60
ctgtcgcccc agctactttg caggctgagc tcaggaggtc aagcctgcct tgggccatga      120
tcatcccatg cactccagcc tgacattcag agcaagacct tgtctcaaag aaagaaaaac      180
atttttatgg tgttttcttt tttagtcttt tcaataatga aaattttcat tttacaggta      240
aaatgaaagg cctggcattt attcaagatc ctgatggcta ctggattgaa attttgaatc      300
ctaacaaaat ggcaacctta atgtagtgtc gtgagaattc tcctttgaga tttcagaaga      360
aaggaaacaa tgtgattcaa gatatttaca taccagaagc atctaggact gatggatcac      420
tgtcccgatt caaattatct ttcagtcctt ttcccccttc tatttcagct ggtccttttc      480
acctaactgt cagtcattct gggtttcaacn atgcttttat tcatgtcctt gaatatagtt      540
ggggcnacttt aattttttang gaataatnna acagnttccn ttaaaggntn ng      592

```

```

<210> 272
<211> 607
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(607)
<223> n = A,T,C or G

```

```

<400> 272
acattaaagt gtgatacttg gttttgaaaa cattcaaaca gtctctgtgg aaatctgaga      60
gaaattggcg gagagctgcc gtggtgcatt cctcctgtag tgcttcaagc taatgcttca      120
tcctctctaa taacttttga tagacagggg ctagtgcac agacctctgg gaagccctgg      180
aaaacgctga tgcttgtttg aagatctcaa gcgcagagtc tgcaagttca tccccctttt      240
cctgaggtct gttggctgga ggctgcagaa cattggtgat gacatggacc acgccatttg      300
tggccatgat gtcaggctcg gcaacaggct ccttgggtgac actcaccaca ttgnttttca      360
agctgacttt cagcttgncn ccttgagag actttaaccc ggaccaaggg cccgatgcct      420
tccgttacct aggaatttca tcaccaatgg tggtaanttca ggaatgttgg caagtttctt      480

```

```

tggcatnttc ccaaanagtt tgttcccggt cttnttggnn ggcangggct tcggaaaggg 540
tttattttgt ngggaaccna aaaactgggg tnaaactcct tnccggttna ngggtttccg 600
nnanccn 607

```

```

<210> 273
<211> 398
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(398)
<223> n = ..,T,C or G

```

```

<400> 273
ggtaccgcca ttattctttt gggcaccttt ggttggtttg ctacctgccg agcttctgca 60
tggatgctaa aactytatgc aatgtttctg actctcggtt ttttggtcga actggtcgct 120
gccatcgtag gatttggttt cagacatgag attaagaaca gctttaagaa taattatgag 180
aaggctttga agcagtataa ctctacagga gattatagaa gccatgcagt agacaagatc 240
caaaatacgt tgcattgttg tgggtgtcacc gattatagag attggacaga tactaattat 300
tactcagaaa aaggatttcc taagagtgtc tgtaaaactg aagattgtac ctgccccggg 360
ccgnccgctc gaaagcttaa ntggccggtt cnaanncg 398

```

```

<210> 274
<211> 587
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(587)
<223> n = A,T,C or G

```

```

<400> 274
actttttttt tttttttttt tttgttgaat caaaagcagg gtttattttt ctatcaaadc 60
cccaatccat gttccagcca atggatgaag ggtgaatcaa gccccacata gactcttggt 120
aaaaacaatt ctaactttct aaaaaaaaaa aaagccaaca cacttttttc tttcttttca 180
aaaagctccc aggccttttg gaacagctga aacaaattca tatcctgact aggtctgttt 240
tctcttaggt atttgatggg tccctctctg ctgccacttc tgcacagatg aggcactgat 300
aatggcctgc aggtcactca caatcctagc tccacatcac tccatgggtt gataacctag 360
aaccacgtta tgatttccat ttataatgcc ctaagaacag ctgaaaagat ctgtattaaa 420
ttctgcaaat ctttattgag tgccactatt tgctgggcac angctaggcn ctggattctg 480
ctggttcttg agaaacctaa aanggnncc tnggccggaa cacccttang gcgaaatcca 540
cncactgggg ggcgtactaa ngggatccaa ctttgggccg acttggg 587

```

```

<210> 275
<211> 588
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(588)

```

<223> n = A,T,C or G

<400> 275

actttttttt	ttttttttt	tttgccttta	taagagaatt	tttattgtta	attattttacc	60
ttaatagttt	cagaaagagg	aacaaattag	ctcagtccaa	catgattggc	agttggcata	120
ttctagttaa	gcaagtgttc	tgactgctaa	ggattttaatt	tggataattt	taatacttag	180
ccatctaaca	cttcaagcat	aaccacagaat	aaatgcacca	ccttcctttc	actttaatac	240
ccgnacctac	ctcacttcga	tataagaaat	atcattcaat	atgattttcca	gaagggacaa	300
gtttcctgga	gaatacaggc	atganggaca	atgcacaaaa	agaaaaactc	aaaatnaaac	360
tctggatgga	taattactaa	gctaaggga	ccaaaccttc	caattttntaa	agaaattaaa	420
tccggttcca	aatgcctnat	angnctatgt	tnaaaagggt	ctggattaat	accggaaaag	480
gnttgnttnt	tacaggatnc	cccaaccgtt	acgggccctt	ngcccagaat	gggccttaaa	540
anccaaagng	tcttttccgn	ngaggcccca	tttnanaatc	cttntttt		588

<210> 276

<211> 595

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(595)

<223> n = A,T,C or G

<400> 276

acttttagata	catcattcct	caaaaagttt	ttaacggaga	aagtggggca	attcaatggg	60
ggaaaggacg	gcctttttta	caaatgggtgc	tggttctact	gggtatctgc	atccttgata	120
cacagaagtt	aactcaagat	ggaccacaga	ctcacatgta	agagctaaaa	taacattcct	180
agaagaaatc	atggaaagtaa	atcttcgtga	ccttgatca	ggtaatgggt	actttttttt	240
tttttttttt	ttttttttta	tcagattaat	tttactttat	ttcttcaggc	ctgggggtttt	300
tcgatgactt	caaatttggg	atcttcaa	ttgaagggtg	gaaatgggtat	tcatgtctgc	360
attaccaaac	atttgctttg	acttaaaaaag	ctcctctcca	gctcttgccg	atctctgaac	420
tagcatcaac	aggntcctcc	agatgtctgg	nccttaaatt	tggattccct	aatcttgccc	480
acaaagangt	ttcttgata	gggaacaaaag	ttcccttatt	naaatgccan	tngtngaacc	540
nccaatgttc	cttcncaaaa	ngggcttaaa	ccggttacc	aattgacaaa	ggaaa	595

<210> 277

<211> 597

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(597)

<223> n = A,T,C or G

<400> 277

ggtactgttc	ctgttggccg	agtggagact	ggtgtttctca	aaccgggtat	ggtggtcacc	60
tttgtctcag	tcaacgttac	aacggaagta	aaatctgtcg	aaatgcacca	tgaagctttg	120
agtgaagctc	ttcctgggga	caatgtgggc	ttcaatgtca	agaatgtgtc	tgtcaaggat	180
gttcgtcgtg	gcaacgttgc	tggtgacagc	aaaaatgacc	caccaatgga	agcagctggc	240
ttcactgtc	agggtattat	cctgaaccat	ccaggccaaa	taagcgccgg	ctatgcccct	300
gtattggatt	gccacacggc	tcacattgca	tgcaagtttg	ctgagctgaa	ggaaaagatt	360

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gatcgccgtt	ctggtaaaaa	gcttggaaga	tggccctaaa	ttcttgaagt	ctgggtgatgc	420
tgccattggt	tgatatgggt	cctggcaagc	ccatgtgtgt	tgaaagcttc	ttaaactatc	480
cacctttggg	tcgctttgct	ggteengatt	tgagacanac	catttccggn	gggtggcaat	540
caaaccattg	ggccaanaaa	gnttntggac	ttgcaagggn	nccaaatttt	ncccaaa	597

<210> 278
 <211> 595
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(595)
 <223> n = A,T,C or G

<400> 278						
ggtacttttt	tttttttttt	tttttttttt	ttagttttatt	aaaataactga	gtttttatttc	60
acatgtatat	ttttgtctcc	ccaccatttc	catgtttgac	caccgctact	actatgtcct	120
atcataacat	tccatacata	cttaaaacca	agcaaagggt	ggagttccat	ctttaaaaac	180
taaacaggca	ttttggacaa	cacattcttg	gcaatagaac	ctggacaaca	tttatcaaac	240
acggtaggga	aagttctcac	tctgcattat	aaaaaggaca	gccagatata	aactgtttaca	300
gaaatgaaat	aagacggaaa	attttttaac	aaattgntta	aactattttc	ttaaagagac	360
ttctccact	gccagagatc	ttgaatagcc	tcttggnacg	tcattccgga	aacaattctt	420
ccataattga	tgaatttggc	tttcactttt	gggaagagaa	cccccttttc	tatacttggg	480
tgcattttgc	ttaaaggctt	ctacaaacta	gggccttttg	gggtttaaga	gttttccngg	540
gtcttgaagg	ntcttggcct	ttgaacttgg	ggtnaaaang	gttgngcttt	tccat	595

<210> 279
 <211> 586
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(586)
 <223> n = A,T,C or G

<400> 279						
ggtacgcggg	gagatacgtt	cgtcagcttg	ctcctttctg	cccgtggacg	ccgccgaaga	60
agcatcgta	aagtctctct	tcaccctgcc	gtcatgtcta	agtcagagtc	tcctaaagag	120
cccgaacagc	tgaggaagcc	cttcattgga	gggttgagct	ttgaaacaac	tgatgagagc	180
ctgaggagcc	attttgagca	atggggaaacg	ctcacggact	gtgtggtaat	gagagatcca	240
aacaccaagc	gctccagggg	cttttgggtt	gtcacatatg	ccactgtgga	ggaggtggat	300
gcggctatga	atgcaaggcc	acacaagggtg	gatggaagaa	ttgtggaacc	aaagagagct	360
gtctccagag	aagatttctca	aagaccaggt	gccacttaaa	ctgtgaaaaa	agatattttg	420
tggtggcatt	naagaagacc	ttgaagaaca	tcaccttaaga	gattattttg	acagtatgga	480
aaattgaaatg	attgaaatca	tgacttgacc	aagcatggcc	aaaaaagggc	tttgctttga	540
accttgagac	atgattcngg	ataaaatgcn	tcaatnct	ntggga		586

<210> 280
 <211> 612
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(612)
 <223> n = A,T,C or G

<400> 280
 actttttttt tttttttttt tttttttcttt tttttttttt tttttttttt ttttgaaaaa 60
 gtcataaagg ccatgggggtt ggcttgaaac cagctttggg aggttcgatt ccttcctttt 120
 ttgtctaaat tttatgtata cgggttcttc aaatgtgtgg taggggtggg ggcatacata 180
 tagccactcc aggttttatgg agggttcttc tactattagg acttttcgct tnaaaacgaa 240
 ggcttntcaa atcatgaaaa ttattaatat tactgctgtt anaaaaatga atgagcctac 300
 anatgatagg atgtttcatg gggngtatgc atcggggtaa tccnaataac gtcggggcat 360
 tccggataag cccaaaaang tttntgggaa aaaaagttn atttaccccc attaaattta 420
 tnnnnaaaag ggattttgcc taagggtggg ctaagggggg ancccngaaa attgggggaa 480
 atcangnaat gaaaccccct ntgatggnaa aaaacagctc ctnttggttg ggccttatng 540
 ggaanngggc ttcaactan naccttnggc ggnaaaaccc ttangngaa ttnnnnncaa 600
 ntgggggggg tn 612

<210> 281
 <211> 593
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(593)
 <223> n = A,T,C or G

<400> 281
 acgctgcttc ttcagagcaa tacgccgccg tttgtgctgc aggacacgtg gagtaacaag 60
 acgctgaatc ttgggtgctt tggctcctagg tttcttacct tctttattta agggctttct 120
 tacaacatac tggcggacat catcttcttt agagagattg aaaagtttgc ggattctgct 180
 agctcttttg gggcccaggc ggcgaggcac tgtagtatca gtcagtcag gaataacctt 240
 ctctcctttt tttacaataa ccaagttgag aacgctcaga ttgcatcca caatgcaacc 300
 acgaactgat tttctctttc tttctcagtt ctcttggtc tgtaacagga atgccctta 360
 ctcaatanca ggcggacacg ggcattgggtc aagacaccct gcttcattgg gaaaccttgg 420
 ttgncgttcc accactggat tcggaccaca taaacctttc attcttnaac caaacgtaac 480
 ancaactttt ggngggccata cncctttata naaagtcggg ggganaagtn ttttgaggga 540
 caagcctgta acnaatagtn aaatcccga tttggattcc taancctttt ccn 593

<210> 282
 <211> 595
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(595)
 <223> n = A,T,C or G

<400> 282
 ggtacaattc aagaaactaa gtatttatgg gcattgaaga aaaaatgttg agataaaatt 60

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gctgtgcaga aaaaagtgtt aatgaagccg acctgactac ttaaccttag agacctgctt 120
tacaagggtg gcccttgatt ggcctctggg aacctggagt tcagggggct tccaccattc 180
ccagaactga tcaaagtagc ttactatatc taaactg.aa aacaatatag tttctcctga 240
acacctgctt tccttctggg agtctggaat tttggtatgt gccaggcaga gactaccttt 300
gtgaccagct cccagtaaaa accccaggca ctcagtcctc aacaagcttt tctggttgac 360
agtgtttcac aagtgcctgtt acaactgggt gctgggagaa ttaagctcat cctctgtgat 420
tccactggcc gaggattctt ggaagcctgc acttaagttt cccctgactt caccctatgg 480
gcttttttcc ttgctgattt ggtttgnatc cttcctgnat aaatcatggc ctgaaccnaa 540
cttgaaaaaa aaannnnnnn nnaaaaaaag gtncttgccc ggcgccgctt naaat 595

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<210> 283
<211> 348
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(348)
<223> n = A,T,C or G

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<400> 283
actttttttt tttttttttt tttttttttt ctattttttt ttttttttgg ctntanaggg 60
ggtanagggg gtgctatagg gtaaatacgg gccctatttc aaagattttt aggggaatta 120
attntaggac gatgggcag aaactgtggt ttgctccaca natttcanag cattgaccgt 180
agtatacccc cggtcgtgta gcggtgaaag tggtttggtt taaacgtccg ggaattgcat 240
ctgtttttta gcctaattgtg gggacagctc atgagtgcaa nacgtnttgt gatgtaatta 300
ttatacgaat gggggcttna atcgggagta cctnggccgn naccacnc 348

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<210> 284
<211> 563
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(563)
<223> n = A,T,C or G

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<400> 284
ggtaccatt aatttgctca gatatagcag gcttaatggt tctatatattt caaaagtttt 60
taagaatggt ttctaacgta ggagagggaa aacatccacc atcccttttc agaattttaa 120
tggagggcag taaacattct ttacacccaa aacctatggc agcagttcaa atttgaccaa 180
ggtaaatgta gaatagagat gttctaaaca cagctaggac tcagcaagtc taacacacta 240
aaatcatatg attacatttt aaaagaaaaat gcacaaaaac caaatagaaa ttttgagatt 300
ttttttcatt tgaaggtaat cttaatgcta ttaaatccac aaatgctaatt ttaaatatcc 360
aatcctattt atctaaaaca cacattgcaa acacacaaat tatctattct ctccacatgt 420
cagccgcccc ttcatatcat ggtttggaat tgggggagaa atagattncc cttaaactgc 480
aagtcaacan ggggttcttt acagttaact ttagccaaat tcataccaaa taccggggtg 540
cctgccnngg cgccggttcn aaa 563

```

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<210> 285
<211> 422
<212> DNA

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<213> Homo sapiens

<400> 285

acaatggact	ggatactaga	aatttttctt	tcactcaaca	gaacataggc	atcctggaat	60
tcacatttct	gaccttttga	tgtattaata	aagtatggag	aaatatagcc	tcgatcaaac	120
ttcatgcctt	caataatttc	taattcatca	ttcagtgttt	ttccatcctt	tactgtgatg	180
acaccctttc	ttccaacttt	tttcattgca	tcagagatga	tattgccaat	ttctttgtct	240
cgttttgtag	aaatcgtagc	aacctgtgca	atttcttcag	gggtgggtcac	aggtttagac	300
tgctttttaa	gttcagcaat	tacagcatca	acagctaaca	tcacacctct	cctgatttcc	360
actggattag	caccttttgc	aatcttctcg	aagccttctt	ggctatagag	cgtgccagta	420
cc						482

<210> 286

<211> 588

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(588)

<223> n = A,T,C or G

<400> 286

actgttcctg	cagggttaagg	caggactgga	actcctccac	agcttgcaca	tagttttcag	60
attcaacact	aactttctccg	agtttaagat	gtgcctgggc	agcataaagc	tgtgcttctt	120
ttgtttcttg	ccttttaaaa	atgatctttg	ctaaatccag	catatcccag	gcaagctcta	180
ggttcccaat	ctcctcctcc	tcattttctt	gaagagactt	gtttttcaagg	actgaatcat	240
ttggcatttc	ttcgggtctta	tcattttctt	tatcatcctc	ttctgagcct	tcagtttcat	300
ctatgtttatc	attattttct	accagagatt	catcttctgn	tnttttctcc	ttcttctct	360
tncacatgca	caccttccaa	ggcgtttcca	acacaccatt	cttcatcttg	ccaacttcag	420
aagtggattt	ccatagaaaa	agaangnttn	ttcacactta	ttaactgctc	ttcatacttt	480
ttacctnaaa	gactaactgn	ttcctggaat	gcattggcgc	ctgctnggaa	atccccatan	540
cngaagtnt	ggcctaanc	aaagtnttta	gttactttcc	catccgac		588

<210> 287

<211> 583

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(583)

<223> n = A,T,C or G

<400> 287

actggaactc	caggaagcgc	tggccagcct	catacgggag	ccatttttct	ttcactgcct	60
ctgctgctga	catcttcttc	tttcccttca	cacctctgaa	gcctatgaag	gctttctgag	120
caggcttcag	cctgggtggc	atgtcttggg	caatcacacc	ctgggagact	gcgtcctgaa	180
gtgacagctt	ctggcccgtg	gttgggtgga	tgatgccacc	tgtgcaggcc	tgagcctcca	240
gaagcctctg	accgctgatg	ctgtcaacga	tgcccgcgtc	tataccttct	gtaatggaga	300
ttttctccag	gttttctgtg	tcaaagatgg	ctgcaatggg	gctcgattct	tncaggggtgt	360
ctgaaaaaga	actgctcctt	atggntaaat	tctgacctg	gatatggtgg	aaatcttact	420
tactgattca	tgtcgggagc	tgctaaaaac	atnatcggtg	caccactggc	catgctgtgn	480

ttgnggccac accatttttn angngacatg taacnaattg antaggtttag nttccgaacg 540
 gaccttggcc ggaacaccta agngatcan ncatggggcg tnn 583

<210> 288
 <211> 607
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(607)
 <223> n = A,T,C or G

<400> 288
 ggtacttttt tttttttttt tttttttggt attttagtttt tatttcataa tcataaaactt 60
 aactctgcaa tccagctagg catgggaggg aacaaggaaa acatggaacc caaaggggaac 120
 tgcagcgaga gcacaaagat tctaggatac tgcgagcaaa tgggggtggag ggggtgctctc 180
 ctgagctaca gaaggaatga tctgggtggtt aagataaaaac acaagtcaaaa cttattcgag 240
 ttgtccacag tcagcaatgg tgatcttctt gctgggtcttg ccattccttg acccaaagcg 300
 ctccatggcc ttcacaatat tcatgccttc tttcactttg ccaaacacca catgcttgcc 360
 atccaaccac tcagtcttgg cagtgcanaat gaaaaactgg gaaccatttg gggttgggtc 420
 cagcattttg catggaccan aatgccagga cccctatgct ttaaggatga anntcttatn 480
 ttnaaatttc tttccataaa nggcttgcca ccaangccat tatngcgngt gaagcaccac 540
 ctgacccata accctggaat aattntnnga aaaccggacc cttntaccna atcttttttc 600
 agggggnn 607

<210> 289
 <211> 591
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(591)
 <223> n = A,T,C or G

<400> 289
 actttttttt tttttttttt tttgagaatg aataagcagt tctttaatgg ttattttaa 60
 atattccaga agagcgttta taattcattt acaagtgcag tattgcgcta gtaaatgtta 120
 cttgacctct tgtataaata atgccgatta agaattagtc ctggaatagt tttcgaattt 180
 ctaactctgt agatctaaaa cacaattgta aatgggtataa agatgtaaga atcatattgt 240
 gataaagtca atctcaaaaa tagagaatcc agacccttcc cagataattt aagaactgag 300
 ttttctctca cttaaacatg atggccacac agaaaacagt aaagacactt ttcgatgtga 360
 taaaactgga taaaactcga gaatatgagt atttagngac caatgnatan acattantgg 420
 aatttttaaaa nccctttttaa tctgaagccg aaaaaaangc cattttccaa gaattattgn 480
 gccctaatac tcatcnannc nngaatannt tncnttcccn ggatagnnnn nnntccnct 540
 tnggaaantg ggcnaantt ntttggntnn aaagggggnc cnttaantcc n 591

<210> 290
 <211> 592
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(592)
 <223> n = A,T,C or G

<400> 290
 ggacttggaa atggttgtct ggaaagcttc cacttttggtc ttgacggcat tcaccctctc 60
 cagcaccttc tcctggattg ctaccccaaa atcattttcca tcttcaatct tggggatcag 120
 gtgttggatc catgtaatca ccagaatgca tttctctttg agagtccaga cttctggctt 180
 aaccagggca agcagggaca ggactttctc attcccaggg agaaatccac acttagggac 240
 ttctttcttc tcctgcttat ctgtttccat ctcattcatcc ttgggtggag ggtctgggat 300
 ggggatgtcc agtggggccc ggaggggaagt caagtcagcc acattgaggg agtcctcttg 360
 caagagctga ttcaggtata tgattttctg tggcaagaat ctgtagagga attcctcanc 420
 ctntctggaaa agaattctgtc tgaagacctt cacttggttg cgggctttcc cgctaagcgc 480
 accccacacg gtttgggcct gctgntttaa tccttaanct ctggcttccg gntagtcccc 540
 cgggaccttg cgggccggcc ntcaaagggc aattcancna ctggcgcccg tn 592

<210> 291
 <211> 609
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(609)
 <223> n = A,T,C or G

<400> 291
 acagtggcat gatctcggct cactgcaacc tctgcctccc gggttcaagc aattctcctg 60
 cctcagccac ccaagtagct gggactacag gtgcgtgcc aacgcgccag ctaaattttg 120
 tatttttagt ggagacgggg ttccaccatg ttggccagga tggctcctaat ctctgaccc 180
 tgcatctgc ccacctcagc ctcccaaagt gctgggatta caggcgtaag ccaccgggac 240
 tggcctgttt tatgattctt aatagttact tggtttaaat cacatttgat actatccttc 300
 tgaaaagtct gagacagatc tacaaactac agtcaaaatt atagattaag aggaatgaat 360
 gcacctatct ggctttaagt tgagatgaa ttattttctca tgctcatttt cttgcngcag 420
 ttatcttaga aagaccccca aaggcttggt attgtaaagc acttgcattga tcacagaatg 480
 caagcttctg gtaccttcgg ccgtgacacg ctaagggcga attcatcaca attgcggggc 540
 gtacctatgg atccannctc ggtccaactt ggcggaatca tgggcatact gnttcctggg 600
 nnaaatgtn 609

<210> 292
 <211> 568
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(568)
 <223> n = A,T,C or G

<400> 292
 actgccaga aggagttcat aaagaatata aagaagaccc caaaagatgt cagcatggca 60
 ctattgaatt cagcagcatc gatgcacaca atggtgtggc cccatcaaga cgtggtgatt 120

tggaataact	tggttattgc	atgatccaat	ggcttactgg	ccatcttctt	tgaggaggata	180
atttgaaaga	tcctaaatat	gttagagatt	ccaaaattag	atacagagaa	aatattgcaa	240
gtttgatgga	caaatgtttt	cctgagaaaa	acaaaccagg	tgaaattgcc	aaatacatgg	300
aaacagtga	attactagac	tacactgaaa	aacctcttta	tgaaaattta	cgtgacattc	360
ttttgcaagg	actaaaaact	ataggaagta	aggggtgatg	caaatggac	ctcaatgggtg	420
tggaatgg	angnttgaaa	gccaaaacca	tnnnnnaaaa	ncttagggcg	aattccannc	480
actggcgcc	gttctaangg	atccagcttg	gncccaactt	ggggtaatca	tgggcataac	540
tggtncttg	ggaaaatggt	ttcccnnn				568

<210> 293

<211> 603

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1) ... (603)

<223> n = A,T,C or G

<400> 293

ggtacttttt	tttttttttt	tttttttttt	ttttttttctt	tttttttttt	tttttngcct	60
ttttaanaaa	cttttatttg	agnggntntt	acaaanattg	nngcaatatg	aaagtcattt	120
gtttgatana	aatacaagc	tgntttgtca	aacacnctga	agtaacccaa	aaatntnttt	180
caaagctcac	anagcttaaa	aagagcnaag	attntntgca	accagacaaa	acctatttnt	240
gcatttctta	tttctttctn	aaactgnttt	gcttaccaaa	ctttnacgtt	taaacatttt	300
caggaaatgc	agggatcatt	ttgtttggaa	ttttaagacc	ccccngaacn	cataggtntt	360
tacaaagaaa	cttttcccgga	tcccttaatt	gaaaagaacc	ntccnaaata	taaantttgn	420
aaactcccnt	ttttggccaa	ttgatcanaa	tgccagaaga	natgctaacc	naanagccct	480
ttaactgggc	tggttattcca	taccctaaan	gggggtttcaa	aactgggttaa	ccttnnccca	540
attttaacct	tngggaaaag	ggnaaaggan	ccccggggna	aaaataaggt	tttgaaaaat	600
aaa						603

<210> 294

<211> 617

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1) ... (617)

<223> n = A,T,C or G

<400> 294

ggtacgcggg	gategettcc	tggctctcgc	cccctccgct	gtctccctgg	agttcttgca	60
agtcggccag	gatgtctcag	gctgagtttg	agaaagctgc	agaggagggt	aggcacctta	120
agaccaagcc	atcggatgag	gagatgctgt	tcactctatg	ccactacaaa	caagcaactg	180
tgggcgacat	aaatacagaa	cggcccggga	tggttgactt	cacgggcaag	gccaaagtggg	240
atgcctggaa	tgagctgaaa	gggacttcca	aggaagatgc	catgaaagct	tacatcaaca	300
aaagtagaag	agctaaagaa	aaaatacggg	atatganaga	ctggatttgg	ttactgtgcc	360
atgtgtttat	cctaaactga	gacaatgcct	tgtttttttc	taataccgtg	gatgggtggga	420
attcgggaaa	ataaccagtt	aaaccagcta	ctcaaggctg	ctcaccatac	ggctctaaca	480
gattaggggc	taaaacgatt	actgactttc	cttgagtagt	tttaatctga	aatcaattaa	540
aagtggattt	tgtaccaaaa	aaaaaaaaaa	aaaaagtnt	gcccgccgg	ccntcaaaa	600

gcnaattcan ccccttg

617

<210> 295

<211> 606

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(606)

<223> n = A,T,C or G

<400> 295

cgagggtactt	ttacccatgaa	catctctaga	ctgtgattat	taaatatagt	gataatatac	60
atggggtttac	tgggatattg	aaaaataaaa	gataatgaac	ccaatttagt	aaatcaacat	120
aaatacaaaa	cagagcgaat	tagccctcta	caactgagct	cgtcctgcgt	cttgagcttg	180
ggttcttttct	ggaactgtct	caaaccttag	tgggggaagt	gaccttatcc	acagattgct	240
tttcccagag	gttccgcttg	ctggatacgt	ctcctgggtc	caagtcagaa	ggtttgggag	300
cagggtgactt	gtttccatct	gggggttttag	ttagccattc	attgatgccg	ctagaaaccc	360
ctaccttcaa	gccagcagtt	tccttatttg	gtgtgcctgc	tgcantgggg	gatgaaaaaca	420
cattcctttc	tnccacatac	tcttggtatg	tgcgtacctg	cccnggcngg	ccgttcnaaa	480
ggccaatttc	acaccactgg	cggccgtact	aatggatcca	aaactcggac	cancttggcg	540
natcatnggc	atactgggtc	ctggggnaaa	tggattccgt	tacattcccc	caacttccag	600
ccnggg						606

<210> 296

<211> 612

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(612)

<223> n = A,T,C or G

<400> 296

ggtacgcggg	gtgccagagg	aaatcttaaa	gcgcctactt	aaagaacagc	acctctggga	60
tgtagacctg	ttggattcaa	aagtgatcga	aattctggac	agccaaactg	aaatttacca	120
gtatgtccaa	aacagtatgg	cacctcatcc	tgctcgagac	tacgttggtt	taagaacctg	180
gaggactaat	ttacccaaag	gagcctgtgc	ccttttacta	acctctgtgg	atcacgatcg	240
cgcacctgtg	gtgggtgtga	gggttaatgt	gctctgtcc	aggtatttga	ttgaaccttg	300
tgggccagga	aaatccaaac	tcacctacat	gtgcagagtt	gacttaaggg	gccacatgcc	360
anaatgggtc	cgcaggaagg	ccgtcaagaa	nggctcgacc	cggntgggtg	ttcaaggaag	420
aaacatttgt	gtcttgggtg	ggaaaaaaaa	tcantgggcc	aactggngga	tgaaagacna	480
tgccggaana	nctgggcttt	ggatgacaac	ccctgcatgg	gcttttgang	ccttaccgcc	540
gatccagggt	tntnttaaca	nggcccggtg	gaatgccnaa	nccccgggta	ctttggagga	600
cccgggtncct	gg					612

<210> 297

<211> 590

<212> DNA

<213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(590)
 <223> n = A,T,C or G

<400> 297
 acgcgggggga acacatccaa gcttaagacg gtgagggtcag cttcacatc tccaggaactc 60
 tccttctttg ggccacggaa ttaaccogag caggcatgga ggctctgct ctcacctcat 120
 cagcagtgc cagtgtggcc aaagtggtea ggggtggctc tggctctgcc gtatgtttgc 180
 ccctggcnag gattgctaca gttgtgattg gaggagtgt ggctgtgccc atggtgctca 240
 gtgccatggg cttcactgcg gcgggaatcg cctcgtcctc catagcagcc aagatgatgt 300
 ccgcggcgcc cattgccaat ggggggtggaa ttgcctcggg caaccttgtg gctactctgc 360
 agtcactggg aacaactgga ctcttcngat tgaccaagtt atcctgggc ttcattgggt 420
 ctgccattgc ggctgcattg cnaggtctac taacttctcg ccttgcctt gcaaaaaaaaa 480
 aaaccttgcc agggaaaaag nccccaancc ttctgaacca accanggggc ccacttttcc 540
 aaaatacctn gggnggaaaa tncecaattt tgantttcnn aggaaanana 590

<210> 298
 <211> 590
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(590)
 <223> n = A,T,C or G

<400> 298
 ggtactttga gccactctcg catggaaagg agtgtcttta tgcctcgacc tcaagctgtg 60
 ggctcttcca attatgcttc caccagtgcc ggactgaagt atcctggaag tggggctgac 120
 cttcctctc cccaaagagc agctggagac agtggtgagg attcagacga cagtgattat 180
 gaaaatttga ttgacctac agagccttct aatagtgaat actcacattc aaaggattct 240
 cgacccatgg cacatcccga cgaggacccc aggaacactc agacctccca gatttaacta 300
 aacaaaagaa actctccacc tagcactgtt tttcttcatt gcttactgag aggggttttg 360
 agaacttaat ctggggggag aactgctttc tcagatcctt aactcccagag aagagaagtc 420
 cttgtgcaca gaacttgtgg gaaccttcat ccgntgtctt tacctttgga tccagtgtgc 480
 aagtttcatg acngaatacat taagatatca aatggcctaa tttggngcna atcatggtat 540
 actgggaaaa ttaggcnaat ggaacttntc accgantttg gtctttaaan 590

<210> 299
 <211> 549
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(549)
 <223> n = A,T,C or G

<400> 299
 cgagggtacaa agatctgaca tgtcaccag ggacccattt caccactgc tctgtttggc 60
 cgccagtctt ttgtctctct cttcagcaat ggtgaggcgg atacccttct ctcggggaag 120
 agaaatccat ggtttgttgc ccttgccaat aacaaaaatg ttggaaagtc gagtggcaaa 180

gctgttgcca	ttggcattcct	tcacgtgaac	cacgtcaaaa	gatccagggt	gcctctctct	240
gttggtgac	acaccaattc	ttcctaggtt	agcacctcca	gtcaccatac	acaggttacc	300
agtgtcgaac	ttgatgaaat	cagtaatctt	gccagtctct	aaatcaatct	gaatggtatc	360
attcaccttg	atgaggggat	cggggtaacg	gatgggtcgg	gcacatgag	tcaccagatg	420
anggatccct	tttgtgcca	caaagatctt	tctactttgc	ancacacact	ggcggncgta	480
ctagtggatc	cacttcgnac	caacttggcg	tatcatgggc	tnactggtnc	cgggggaaat	540
ggtatccnn						549

<210> 300

<211> 591

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(591)

<223> n = A,T,C or G

<400> 300

actccagcct	gggcgacaga	gcaagactcc	acctcaaaaa	agaaatattt	agcaaattatt	60
aaaggacaag	aggggaatatt	tgtttaaaaa	attataatgc	acgttagatg	aaaagtaata	120
ggatgagatg	gttggtgctg	aaatagcact	tgctatataa	attcaaacat	tcctttttcaa	180
attcagcttc	tcagagggtt	gacttcagat	gcttgagcac	tttcaacatt	atctttgcct	240
ttatccttcn	ttatgcggat	aaacacaact	gctaaaatta	taccattgat	tttggaact	300
tcccagtcgt	tttgtaagct	tcactgccga	gggaaaatgt	aaaatgggga	ccccgaaata	360
aagtgtgat	catcatcaag	tagcctcgaa	aatgagactt	tcagggtgcac	tgaaggggat	420
ggcagaagaa	caagccccgt	gtagtccttg	ctagcctggg	aagggtggca	ttcacatcct	480
taaggatcan	gtggactttg	acnccgaact	taaaggaaga	accccttatt	ntggggccac	540
cacttgacct	tgggcccggaa	cacccttaag	gcgaattcca	cacactgggg	g	591

<210> 301

<211> 655

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(655)

<223> n = A,T,C or G

<400> 301

cgagggtactc	tttaaaaagg	gactgcaggg	ctgggtgtag	tggctcacac	ctgtaatccc	60
agcacttttg	gaggccaagg	caggtgggtc	acttgaggcc	aggagtttga	gaccagcctg	120
accaacatgg	caaaacccca	tctctatcaa	aatacaaaaa	ttagctgggc	atgatggtgc	180
actcctgtaa	tcccagctac	ttggtaggct	gaagcatgag	aattgcttaa	acctgggagg	240
cagaggttgc	agtaagccaa	gatcatgcca	ctgcactcca	gcctgggcaa	cagagtaaga	300
ctctgtctta	ataaataaat	aagaaaataa	aacggaactg	cagtgcctaac	agtaatttat	360
acatttttaa	atgttctgag	tatgttttga	ctgggctagt	gtaacaatat	actaccctga	420
aaagtgcagt	tttgattgtt	ggtggtgtct	ttgggtcang	aaaagtgaac	tgtgccaaga	480
agtatttttc	aatgacatga	atggatttct	gttaatgcaa	ttgactgaga	aaatgngctt	540
acgctttctt	aactgcaaaa	agagntttgt	ccacatcana	attgttgaaa	ctggngctgt	600
ttctgttgcc	tgggatctga	tgactgggat	ttcctcttgg	acaaaanacc	tgatn	655

<210> 302
 <211> 513
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(513)
 <223> n = A,T,C or G

<400> 302
 actcgtcttg gtgagagcgt gagctgctga gatttgggag tctgcgctag gcccgttgg 60
 agttctgagc cgatggaaga gttcactcat gtttgcaccc gcggtgatgc gtgcttttcg 120
 caagaacaag actctcggct atggagtccc catgttgatg gatcctgagc ttgaaaaaaa 180
 actgaaagag aataaaatat ctttagagtc ggaatatgag aaaatcaaag actccaagtt 240
 tgatgactgg aagaatatcc gaggaccag gccttgggaa gatcctgacc tcctccaagg 300
 aagaaatcca gaaagcctta agactaagac aacttgactc tgctgatttt tttttccttt 360
 ttttttttta aataaaaata ctattaactg gacttcctaa tataacttc tatcaagtgg 420
 aaaggaaatt ccaggcccat ggaaacttgg atatgggtaa attgatgacc aataatcttc 480
 acttaaagnc atgtcctttg gccgcgaaca cgc 513

<210> 303
 <211> 610
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(610)
 <223> n = A,T,C or G

<400> 303
 acgcggggct tgcagagccg gctccggagg agacgcacgc agctgacttt gtcttctccg 60
 cagcactggt acagaggtct ccagagcctt ctctctcctg tgcaaaatgg caactcttaa 120
 ggaaaaactc attgcaccag ttgcggaaga agaggcanca gttccaaaca ataagatcac 180
 tgtagtgggt gttggacaag tnggtatggn gtgtgtatc agcattctgg gaaagtctct 240
 ggctgatgaa cttgctcttg tggatgtttt ggaagataag cttaaaggag aaatgatgga 300
 tctgcagcgt ggggagctta tttcttcana caccttnaaa ttgtgggcag atnaagatta 360
 ttctgtgacc cgtcaattct tanattngta gttggttact gcatggaatt cngtcagcaa 420
 gaaangggaa aantctngtt caatttggtn gnataagaan tggttaatgg tcttcaaatt 480
 cnttattcct tcagancggc caagtacctn ggccnganc atgcctaagg gctaattcna 540
 ctcantgng gccgntctan ntggattcca ncttgggtacc aancttggng ntattnatgt 600
 caatanctgg 610

<210> 304
 <211> 596
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(596)
 <223> n = A,T,C or G

<400> 304

ggtacctgga	attatcta	att	tggccagagg	tggcgcccga	cccatcagtt	cgaaatgtag	60
aagtaataga	gttggcaaaa	gaatggaccc	cagcaggaaa	agcaaagcaa	gagaattctg		120
ctaagaagtt	ttattctgaa	tctgaggaag	aggaggactc	ttctgatagt	agcagtgaca		180
gtgagagtga	atctggaaa	tgaaaagtgg	agaacaaggc	cgaaagtggg	ggaggaagga		240
gacagcaatg	aggacagcag	tgangactcc	tncagtggagc	angacagtga	gagtggacgg		300
gagtcaggcc	tagaaaacan	angaacagcc	nagangaact	caaaagccaa	agggaaaaag		360
tgattctgaa	gatggggaga	aggaaaatga	aaaatctaaa	acttcagatt	cttcaaata		420
cgaatctagt	tcaattanaa	gacagttctt	ccgattcttg	aatcagaatc	agaacctgaa		480
agtgaatctt	gaatncngaa	cagtcgctta	ggagaaagaa	agaaaccaag	caggattgac		540
tcctttttnc	aagntgttcc	ttctaaactg	gatgatttaa	ccngntccct	cagtgn		596

<210> 305

<211> 629

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1) ... (629)

<223> n = A,T,C or G

<400> 305

ggtactttnt	tttttttttt	tttttttttt	tttttttttt	tggggattta	ntttttattt	60
cataatcata	aacttaactn	tgcaatccan	ctaggcatgg	gaggaacaa	ggaaaacatg	120
gaacccaaag	ggaactgcag	cgagagcnca	aanattntng	gatactgcga	gcaaattggg	180
nggaggggng	ctntcctgag	ctacaaaagg	aatgatctgg	tggntaaaat	aaaacacaag	240
tcaaacttat	tnnagttgtc	cacagncagc	aatggngatc	ttcttgctgg	ncttgccatt	300
cctggacceca	aagcgctcca	tggcctccac	aanattcatg	ccttctttna	ctttgccaaa	360
caccacatgc	ttgccatcca	accactcant	cttgggnagng	cagatgaaaa	actgggaacc	420
atttttnttg	ggtecnacat	ttccatggca	aaangccang	accnttgct	ttaagaagaa	480
aatctcatct	tcaaattctn	ccctaaanga	cttgccncan	gccntntggg	tgngaagcnc	540
cccctgncca	taaccctgga	tatttttgaa	agaggancct	ntacnaacnt	ttttccnggt	600
aanaaaaaat	ttttnttttg	acctnccca				629

<210> 306

<211> 643

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1) ... (643)

<223> n = A,T,C or G

<400> 306

acagggagga	atttgaagta	gatagaaacc	gacctggatt	actccggctc	gaactcagat	60
cacgtaggac	tttaatcggt	gaacaaacga	acctttaata	gcggctgcac	catcgggatg	120
tcctgatccc	ccgcgtacat	ttccttgtag	actctgttaa	tttctgcag	ctcctgggtg	180
gttctggagc	agatgatctc	aatgagagag	tcctcgctcg	ttcccagccc	cttcattgga	240
gcttttatct	cagaagcgct	atactgagca	ggtgtnttca	ataggcccaa	aatcaccgtc	300
tccaggtggc	cagataaggc	tgacttcaat	gctgatgcaa	gntccttttt	ggtccttctc	360


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tggtaggcga aggnaatatc ctgtctctgt ncattgcttg cggntgggca aaatgttgac      420
aatggtgacc tcatccacac ctttgggtctt tgatggntgg ntcaatgttc aaagcatccg      480
ctcagcatca aaantaagta tangctttgc agaccatata gcacttgggg gngnngagng      540
acaccctcca actgaacttg ccaggatttn tgaaagtaan anttttaaga acttgccgnc      600
cccanactaa acnnccaatc tagcccnntn cctaacggcc aag                          643

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<210> 307
<211> 643
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(643)
<223> n = A,T,C or G

```

```

<400> 307
cgaggtactt tttttttttt tttttttntt ttnttntnnn tttggggatt nantttttat      60
ttcataatca taaacttaac tctgcaatcc aactaggcat gggagggaac aaggaaaaca      120
tggaacccaa agggaactgc ancgagagca caaanattct nggatactgc gancaaatgg      180
ggngggagggg tgctctcctn agctacaaaa ggaatgatct ggtgggtaan ataaaaacaca      240
agtcaaaactt attcnagttt tccacagnca gcaaagggga ncttcttgnt gggcttgcca      300
ttcctggacc caaaacgctc catggntctc caaaatttat gccttttttt actttgcca      360
anaccacatg ctttgcttcc caccnctcan tttttgnngg ggnaataaaa aancgggaac      420
cnnttggtgtt tggncncaaa ttttcctntg gnaaaaaacc ncgacccttt tntttaagaa      480
naaaattttta ntttttaaaat tttcccctaa aaaggactgg ccnaaggcn ttttgggggn      540
gaagcccnc nccccnaaa cctggaaaaa ttttggaagc nggacccttt accaaatctt      600
tntcctgggtt aaaaaaaaaa tttttttttt gacctttccc aan                          643

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<210> 308
<211> 653
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(653)
<223> n = A,T,C or G

```

```

<400> 308
cgaggtacag agagtagctt ctgtgatgca agaataact cagtcaggtg gtgttcgtcc      60
atttgagatt tctttactta tttgtggttg gaatgagggg gaccatatt tatttcagtc      120
agatccatct ggagcttact ttgcctggaa agctacagca atgggaaaga actatgtgaa      180
tggaagactt ttccttgaga aaagatataa tgaayatctg gaacttgaag atgccattca      240
tacagccatc ttaaccctaa aggaaagctt tgaagggcaa atgacagagg ataacataga      300
agttggaatc tgcaatgaag ctggatttag gaggcttact ccaactgaag ttaaggatta      360
cttggtgccc atagcataac aatgaaagtg actgaaaaat ccagaatttc agataatcta      420
tctacttaaa catgttttaa agatgggttg tttgcaagac tttttgcata cttanttcta      480
catgaattaa atcactgggt tnaaatgaca cttattaatc ctaataactg gtnaaccnc      540
aaaaaaaaa aaaaaaaaaa ntacttcccc ggcggcgcgc gaanggcaat tcacnctgg      600
cggccgtcta tggatccacc cggncacact gggnaacagg cnactgggtc tgg                          653

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<210> 309

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<211> 649
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(649)
 <223> n = A,T,C or G

<400> 309
 acttgcaaaa gcacttgaag tcattaaacc agctcatata ctgcaagaga aagaagaaca 60
 gcatcagttg gctgtcactg cataccttaa aaattcacga aaagagcacc agcggatcct 120
 ggctcgccgc cagacaattg aggagagaaa agagcgcctt gagagtctga atattcagcg 180
 tgagaaagaa gaattggaac agagggaagc tgaactccan aaagtgcgga aggctgagga 240
 agagaggctg cgccaggaag caaaggagag agagaaggag cgtatcttac aggaacatga 300
 acaaatcaaa aagaaaactg tccgagagcg tttggagcag atcaagaaaa cagaactggg 360
 tgccaaagca ttcaaagata ttgatattga agaccttgag gaaatggatc cagattttat 420
 catggctnaa cagggtgaac aactggagaa agaaaagaaa gaacttcaga acccttaaga 480
 atcagaaaag aagattgctn ttttgaagac ccacctttgg aaaaattcct ttgttaagag 540
 cctttcgagg acagaaaatt aagacatggg ctggggngcc cccgaggaga aagaattctc 600
 ctgcccttga cgtgaaaggt nttgcataaa atcatgtccn atcttgaga 649

<210> 310
 <211> 319
 <212> DNA
 <213> Homo sapiens

<400> 310
 cgaggtaacta gccggacttg gattttcttg aaagatttca gttgaggaac gggaacaag 60
 attatgatag ctttcgacc accaccaact tcaatttcct tagctgccgt aatattcagc 120
 tccctgagct gagccttgag gtccgagttc atctccagct ccagaagagc ctgggagatg 180
 cgggactcga actcgtccgg cttctcgcca ttgggcttca cgtatctggc gctcgaaactg 240
 aacatggctt tctcctggga gaacttgccg agcgccggct taggaagaga ccccgctac 300
 ctgccgggcg ggcgctcga 319

<210> 311
 <211> 646
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(646)
 <223> n = A,T,C or G

<400> 311
 cgaggtaactg atgcaacagt tgggtagcca atctgcagac agacactggc aacattgcgg 60
 acaccctcca ggaagcgaga atgcagagtt tcctctgtga tatcaagcac ttcggggttg 120
 tagatgctgc cattgtcgaa cacctgctgg atgaccagcc caaaggagaa gggggagatg 180
 ttgagcatgt tcagcagcgt ggcttcgctg gctcccactt tgtctccagt cttgatcaag 240
 ctgcacatca ctangattt caatgggtgcc cctggagatt ttagtggtga tacctaaagc 300
 ctggaaaaaa ggaggtcttn tntggcccca aaccaatgtt ctgggctggc caatgacttc 360
 acatgggggca atggcaccaa caccggcaga acttgnaccc tattgccaca acatgtcctt 420

```

atctnaatga nggncttctt tgtgaaaaca aaccccatc cccggaatta agnacaantt      480
cttcaaactt ggggtgnttc aagggcctcg atngcctgcc catatnggtt ttttgccata      540
aaacacaacn ttccnnaaag gaatccgant nttgttttgt tggancccat ttttgttccc      600
aagaaaattn ggtaatatcc aaattgggga attaggaaaa tgggnt                      646

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```

<210> 312
<211> 622
<212> DNA
<213> Homo sapiens

```

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<220>
<221> misc_feature
<222> (1)...(622)
<223> n = A,T,C or G

```

```

<400> 312
cgaggtactt ttgtgagagg gttcaatggg agagctttaa tgcagatgag acttgaagct      60
tctgaagaag atctaagtct tgatgagggt attcaaactc aaatcttgaa tgcataatga      120
tgataggcca tgggtcttcaa aaacgtggta cttttaatag caacagggtt tcaccatggt      180
ggccaggctg gtctcaaatt cctgacctca agtgatctgc ccacttaagt gctgggatta      240
caggcatgag ccacaacatc tggccagaaa tattttttct tttctttctc tttctctctc      300
tctttttttt tttttttttt tttggagctc gctctgtccc ccagctgcaa tgcaatgggg      360
caatcttaac ttactgnaac ctccccctcc aggtcnaaag aatctttgng ctacctccta      420
natntnggaa tacaagggag tccccacctc actaattttg ntttttaaga aaaggagggt      480
ttancatggt ggtngntga tcccaacctc cgaccttaan gancctccgc ctaatttcca      540
aaggctggat nttggctgan cccacccenc ttaaccacaaa ttnaaattct tttntcctgc      600
cgggggagct aaagggaatc aa                      622

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```

<210> 313
<211> 674
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(674)
<223> n = A,T,C or G

```

```

<400> 313
nggacttgaa atcattgaag ttctgcaaaa aggagatgga natgcacaca gaaagaaaga      60
tacagaggtc cgcagacggg agctcctaga atccatttct ccagctttgt taanctacct      120
gcntgaacac gcccaagacg tgggtgctaga taagtacagc tgtgngtagg tntctgncat      180
tccngggaac agacnaattn gaccatnagg naacctgagc ttnccaaagt ncgcaaggct      240
gaagaagana ggctnctcca ggaagcnnac gagaaagana aangagccgt attttacnag      300
aacatgaaca aatcaaaaaa naaaactgtc cgaaaaccgt ttggagcaaa ncaaanaaaa      360
cagnacctgg gngcccaaag cattcnaana tatttggtat tancncaccn tgatggattc      420
naaacnttat ttttncttgg cncggctggg ccgcccggct ngngnaaaga aaagaacttt      480
nctaccnctc ccgaatcaag aaaagaanat ggcttttttn taaaanncaa cccttgggaa      540
aaaattcttt gtttaananc cctccaangc ccgggaaatt aattcatgct ttgtgtgngc      600
gacnannaa aaaanaanan atccttcctt ccccttaann gaaaagggcc ttncacaaaa      660
tgattgccca agnc                      674

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```

<210> 314

```

<211> 646
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(646)
 <223> n = A,T,C or G

<400> 314

actttttttt	ttttttttt	ttttttttt	tttgagatgg	agtcttgctc	tgctgcccag	60
gctggagtgc	agtgttgcca	tctcagctca	ttgcaacctc	tgctcccag	gttcaagtga	120
ttctcctgcc	tnagcctcct	gagtagttgg	gactacaggc	acatgccacc	atgcctggct	180
aatttttttg	cattttttaag	tanagacagg	gtttcatcat	gttgccagg	caggtntcaa	240
actcctgacc	tcaagtgatc	cacctgtctc	agcctcccaa	agtgtctgga	ttacaggcat	300
gagccactgn	accgggccta	aaaatgatta	cttcttataa	aaaggatttc	ttccccttca	360
caacacttan	cttccttttt	ctttcctggg	aactatgggt	ntggngnccg	cataaggatc	420
taccttnenc	aagctggaca	ntgggggttg	ctncttgang	gnaactcagg	ccanatacng	480
accctggggg	gaacnctaaa	cttacttggg	tanaaccggg	gctaacattt	ctgcttgnga	540
ngttgattcc	ccncaaattt	ttaaaagggn	tttcatggcc	cttagggcaa	ccattttaca	600
aagatgggnc	acatgggnctt	ggccgnaacc	cctangngaa	ttcnncn		646

<210> 315
 <211> 666
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(666)
 <223> n = A,T,C or G

<400> 315

acagtccttg	gatatttagg	aaggggatgg	ggagaaagtc	agttctcaga	acaaattagt	60
cagcttcagt	ctcgtcagca	gggtctttgg	attctttggt	cttccgcact	tcttcaatgt	120
gcttatcctt	ctctcgcaa	cgttccagtt	tggcagccat	ttgtgcctct	cggttctctt	180
tattagcttc	cattttgtgg	gtcagtttct	cttctgccat	tttactgaag	ttgntgttct	240
cttctattgc	cttctgaagc	acttctttct	cgtgctctcg	tttctcancc	agctgcttca	300
agaccttagc	ttcatgggac	ttgcgtcttt	cttctgcagc	ttctaatttc	ttctgaattt	360
cctccaggga	aagaccttct	tctttggaag	ggaaaggggg	aattctggaa	ccagattctt	420
ttgacccaag	gctgaaaatc	agcttaaaaag	cctggccttg	angcaccnt	tttcagntct	480
ttcacctgga	tatcntaaaag	aagccctngt	gattnaaaac	aagccnaccg	gcantnnatt	540
ntgncaanan	cnnggataan	gnaatccctg	tnaantccna	ccccnacc	cattttcccg	600
ggaccttggc	ngnaaccctt	tanggngaag	tcnncnctn	ggcgcccgta	ctaangggac	660
ccaccg						666

<210> 316
 <211> 656
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature

<222> (1)...(656)

<223> n = A,T,C or G

<400> 316

actcttggtt	tgtcaatggg	actttccagc	aatccaccca	agagctcttt	atccccaaca	60
tcactgtgaa	taatagtgga	tcctatacgt	gccaaagcca	taactcagac	actggcctca	120
ataggaccac	agtcacgacg	atcacagtct	atgcagagcc	acccaaaccc	ttcatcacca	180
gcaacaactc	caaccccgtg	gaggatgagg	atgctgtagc	cttaacctgt	gaacctgaga	240
ttcagaacac	aacctactgt	gggtgggtaa	ataatcagag	ccttcccgcnc	aagtcccagg	300
cttgcaactg	gccnatgacc	aacaggaccc	tnactctact	tagtgtcaca	aggaatgatg	360
ganggacct	atgaagtgtg	gaaaccagaa	ccaattaagt	ggtgnccaca	cganccaggc	420
attcttgaat	ggcccttatg	gnccanaaga	acccaccatt	tcccctnata	cacctaattc	480
cgtccagggt	gaaccttaag	ctntctggca	tgcaancctt	aaccactggc	aggattcttg	540
gnttaatgaa	gggaacattc	nnacccnccc	agaagttttt	attttcaact	tacttggaan	600
aacgggggct	ntttactgcc	ngccataact	taacnggggc	cnnancggac	ttcggn	656

<210> 317

<211> 636

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(636)

<223> n = A,T,C or G

<400> 317

actttttttt	tttttttttt	tttttttttt	tttgnagtca	gctattttaat	taggttctta	60
agacatttag	aacaccaatt	tgngaggata	aattccattc	gtcagagcaa	acacagatcg	120
caggtagccc	tggagctgag	gaatagcttt	gatttttggg	aaaatttgtg	agtccacagc	180
tttctgatca	atcttgctgt	gctccgtaat	ctcatatttc	cctttttctg	ggncgaaaan	240
cttacctttc	tggggnttgg	gcttncgcag	cttcttcttn	ttgaagtaag	catnagtaan	300
aagntttggg	anttttacan	tgntgatann	catttttgnt	gaagnggnan	tgacnaattt	360
ctgggggggt	cttcgtaaag	gaactcnant	gaggcccaag	ggncctgccc	agtaataaag	420
ccctnncanc	tggttangga	aacccccctn	tggcctgggg	ggncctgccc	gntgatccaa	480
atggcccccg	ggaaaagcng	gntcaanttt	tnacggctnc	tnaaagggtt	ttgccnggnt	540
taancttttn	ggncnttttc	agnggaaana	ccngctttgn	nantntaccc	ccggnctctc	600
ggcggaaacc	nttaggggna	attncncnct	gggggg			636

<210> 318

<211> 654

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(654)

<223> n = A,T,C or G

<400> 318

cgaggtagcg	ggggcctttc	tgcccgtgga	cgccgcccga	gaagcatcgt	taaagtctct	60
cttcaccctg	ccgtcatgtc	taagtcagag	tctcctaaag	agcccgaaca	gctgaggaag	120
ctcttcattg	gagggttgag	ctttgaaaca	actgatgaga	gcctgaggag	ccatttttag	180

```

caatgggggaa cgctcacgga ctgtgtggta atgagagatc caaacaccaa gcgctncagg      240
ggctttgggt ttgtcacata tgccactgtg gaagagggtg atgcagctat gaatgcaagg      300
ncacacaagg tggatggaag aattgtggaa ccaaagaaaa ctgtcttcag agaagattct      360
taaagaccan gtgccactt aactgtgaaa aagatatttg gtggtggcat taaagaagac      420
atgaagaac atcactaaga gantattttg aacagtatgg anaaaattgn agngattgaa      480
atnatgactg ccnangcagt ggcancaaan ggggctttgg ctttnnacct ttgacnacca      540
tgactcnngg ataaaatggn attcnnaaat cctcntgng aatggccnca ctgggaagtt      600
ngaaancctn ncaacnagaa agggtncgnt tnntcncca aangcnaang tttc          654

```

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<210> 319
<211> 659
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(659)
<223> n = A,T,C or G

```

```

<400> 319
acgcgggggaa gccaaactcag actcagccaa cagagattgt tgatttgcct cttaagcaag      60
agattcattg cagctcagca tggtcagac cagctcatat ttcattgctga tctcctgcct      120
gatgtttctg tctcagagcc aaggccaaga ggcccagaca gagttgcccc agggcccgat      180
cagctgcccc gaaggcacca atgcctatcg ctctactgc tactacttta atgaaagacc      240
gtgagacctg ggttgatgca anactcttat tgncagaaca tgaattnngg caacctgggtg      300
tctgtgctna cccangccca aggtgccctt ggggctcac tgattaanga aantggcact      360
gatgacttca atggctggaa tggccttcat gacccnaaa aagaacccgc gnttgcaactg      420
gacagtgggt cctngntct cttacaagtc tggggcaatt ggancccaa nccatgntaa      480
ttcnggctac tggggtgagc nnacctcagc ccaggatttn gaantggaan gcctgncttg      540
ggaanacaag ttcttcttn gctngcaagt tcaaaacctt atgcagctgg aaaatcatnt      600
ctanaactga tcagcattcn accgnttcaa attaaccggc ctttttcant tanttaccg      654

```

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<210> 320
<211> 664
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(664)
<223> n = A,T,C or G

```

```

<400> 320
ggtactctgc cttttaggag atgaggtaag acatatacat agatggcttt tactagccaa      60
ggcaatgtaa atggactaag attctcatgt gacttgaggt tatctgatga atttattctc      120
ttcaaaacca cctactttta gagggcatgt ttaaccctc tctttattta aggagggaga      180
gaaaaacaca tgtaaccaga attcagagtg ggttactcaa cctaagagaa catacggagt      240
tctctttggg aaaacgacaa gactacagtg ttcacttcgc accatgaagt ggcactcctg      300
ntatggctgc agantcctct tacttcttat gaaaggatgc atctgattct gaaattactg      360
atatattcga tcagttaggg atgntttaaa aagnaaaaac caatgccaca catacacttt      420
ctagctttct gaaaatnacc cgacacattn ccnaaaatng agaatttacc ctattacttt      480
tagagaaatt tccataatat tcttgggtaa agaancnng ttgggcatat tnccaatttt      540
cagngnctnt ggttttatgc ccnaganccc aataggntcc cccatttttt aaggcttttt      600

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ccacngacga ttttttaaan cnttctnnan tgggggaaga ataatcttaa aagtnngnctt 660
atnt 664

<210> 321
<211> 666
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(666)
<223> n = A,T,C or G

<400> 321
cgaggtacag tattacagtc agccacagaa gctgtgttgg gggacaagac ccaatccttc 60
cccacaccag gcaaagcagt attggacatg agttggcatg tggctgggcc cacgtcctta 120
tccccaggc ctgaggggag accaccttct gatgataacc aacccttagc taccactctg 180
tattcatcag gggaggggta taaacccgc atgcaagaag aacccttgcc cccagtgtca 240
aatgggatgg ggatgctaga gttatagtaa aggggaaacc ctatgtaagc tgntaacaga 300
gttcacaggg gtagggataa cccctgntct tcagctncca aatgngctca cttccagct 360
tcttcatccg tcatcaatgc tggcaaagtt tccctnaact gnggccaggt tttcacgcat 420
gggtggctgc acctgggtca aaaaggtggn attggcctnt aaggaattag caatcatntg 480
ctgggtggga ttccagtgtg taaggaactt anccaactgc atggnttgnt tgtgcanctg 540
cttgatggng acaagttnt gcaccanctn aaggaagggtg gaagcatggg gctcaacctn 600
gataagttca tatacttggg gnccttgct ttgggatctg catntttaca aggnntatcn 660
tgcan 666

<210> 322
<211> 631
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(631)
<223> n = A,T,C or G

<400> 322
accggaaagg aagctcccat tcaaaggaaa tttatcttaa gatactgtaa atgatactaa 60
ttttttgtcc atttgaaata tataagttgt gctataacaa atcatcctgt caagtgtaac 120
cactgtccac gtagttgaac ttctgggatc aagaaagtct atttaaattg attcccatca 180
taactgggtg ggtacatcta actcaactgt gaaaagacac atcacacaat cacccttctg 240
ctgattacac ggcctggggt ctctgccttc tccccttacc cttccggctc cacccttct 300
gcaacaacag ccctntacct ggggggcttg ntagaagaga tgtgaagggt tcaaggctgc 360
aacctgtggg actactgcta ggtgtgtggg gnggttcgcc tgcaccctg gggtctttaa 420
gncttaaaagt gatgcccctt tccaaccatt attctggnc cactctctc actccggcct 480
tggncnanca taaatgnacc ccttcacttc ctntgagaat ggccttcgng aagaatcnag 540
gctttcccaa ncttctttcc cccnttctc angggngctg gttttctnct ctcaagggtc 600
ntttgaccgn accaccaaac ttctgaattn t 631

<210> 323
<211> 647
<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(647)

<223> n = A,T,C or G

<400> 323

actgtgggtc	gaagtaatgg	atacggacgt	aaccatcttc	gccgccgctg	ctgtagctct	60
tgccatcagg	atggaaggca	acactgttga	taggtccaaa	gtgacccttg	actcttccaa	120
actcttctc	aaaggccaaa	tggaagaacc	tggcctcaaa	cttgccaatc	ctgggtggagg	180
ttgtgggttac	atccatggct	tcctgaccac	cgcccaggac	cacatgggtca	tagttggggg	240
agagggcagc	tgagttgaca	ggacgtttctg	tccggaaagt	cttctgatgt	tcaagagttg	300
tggagtcgaa	aagcttggct	gtgttgctct	tggacgcggt	cacaaacatg	ggcatgtccc	360
tggataactg	gatgtccgtg	atctgcccg	agtgtctctt	aacattncca	acacctnttc	420
aaanttggca	ctatactggg	tgagctcttc	acttttatng	gcaacgnatg	atcacttccc	480
caaggggtccc	caaacagcac	tggggaattt	agagncattc	cagggaaactt	tatgtagggt	540
tcattggtgca	attggttnga	tcccagggtc	aaaaagttnc	aaacactgga	nccctttctt	600
gtccnnggag	aacatgttat	ttgccccaa	taaaaccng	nccgng		647

<210> 324

<211> 653

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(653)

<223> n = A,T,C or G

<400> 324

ggtacttttt	tttttttttt	tttttttttt	ttgagatgga	gtcttgctct	gttgccagac	60
cggagtgcag	tgggtgcgatc	tgggctcact	gcaatctcca	cctcccgggt	tcaagcgatt	120
ctcctgcctc	agcctcccga	gtaactggga	ctacagggtg	gcgccaccaa	gccagctca	180
tttttgatt	tttagtanag	atgggttttc	acgatgttgg	ctaggatggt	ctcgatctct	240
ggtcagagtc	ttttctgtaa	aaatccttgg	taaagaagca	attttagact	gtancctgtt	300
gcaaatgcnt	taaggaagaa	gcaaaacaac	tgntagtctt	tctgaaatga	aaaaactacn	360
ccagggctgg	tatatnnaga	gcaaccccaa	ccannactnc	catcntgatg	cccacagggg	420
cccactgana	naccngaaa	angtcnnaa	gcntaaannt	ngangcnttg	cttttgaaat	480
attgcgcng	taccnagntn	nagacaaacn	ngnttaaggc	ccnnantntt	tggccngant	540
ttgcgataaa	aaaaacttgg	gggtcgctnc	nngatcccn	ttgtncacca	naantctggg	600
ggatgggttn	aagcccntgn	cnnaagggtt	nngttctccc	aaggtaaaaa	nng	653

<210> 325

<211> 655

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(655)

<223> n = A,T,C or G


```

<400> 325
ggtagcgggg gccttttggc tctctgacca gcaccatggc ggttggcaag aacaagcgcc      60
ttacgaaagg cggcaaaaag ggagccaaga agaaagtggg tgatccattt tctaagaaag      120
attggtatga tgtgaaagca cctgctatgt tcaatataag aaatattgga aagacgctcg      180
tcaccaggac ccaaggaacc aaaattgcat ctgatggctc caaggggtcg tgtgtttgaa      240
agtgagtctt gctgatttgc agaattgatga agttgcattt agaaaattca agctgattac      300
tgaagatggt caaggggtaaa aactgnctga ctaacttcca tggcatggat cttacccgtg      360
acaaaatgtg gtccatgggc aaaaaatggc agaccatgat tgaagcttac ggtgatgtca      420
agactaccga atgggtactt gcttcgtctg gtctgggggtg ggtttactaa aaaacgcaca      480
atnanatacc gaagaactct tatgcttang accacangtc cngccaatcc ggagaanata      540
tggaatctg accccaaagn gccnaccaat gacttgaaaa annggccatt aaatgggtcn      600
nacacnttgg aaaagcctta aaaggttgcc aantattaac ctntcatgaa gnttc      655

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<210> 326
<211> 657
<212> DNA
<213> Homo sapiens

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<220>
<221> misc_feature
<222> (1)...(657)
<223> n = A,T,C or G

```

```

<400> 326
ggtagcgggg ggaaacggga gtgaacggag agcgtagtga ccatcatgag cctcctcaac      60
aagcccaaga gtgagatgac cccagaggag ctgcagaagc gagaggagga ggaatttaac      120
accggtccac tctctgtgct cacacagtca gtcaagaaca ataccaagt gctcatcaac      180
tgccgcaaca ataagaaact cctggggccgc gtgaaggcct tcgataggca ctgcaacatg      240
gtgctggaga acgtgaagga gatgtggact gaggtacttt tttttttttt ttnttctttt      300
ttttgagata ggnctcact gnatnaccca ntntggaatg caattggcat gaacncagct      360
tactgnagnc ttccaaacct gggctcaagc aattatnttg nattaacctn ttgagtacct      420
gggactntcn cangcaccan ccctgctttg cttacttaaa tttttgtnaa nacnnggctt      480
gctttttttc ccaggntggn tcnactccn gaattaaggg atccttcccc ctcaattttt      540
aaannngctg ngattntnga atangccttt ttgttngccc ttttnacctt ttnnnngggt      600
nnttcnnggc tttaanctn ccggggggccn tttaaaggng aaatcncncc ttggggg      657

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```

<210> 327
<211> 658
<212> DNA
<213> Homo sapiens

```

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<220>
<221> misc_feature
<222> (1)...(658)
<223> n = A,T,C or G

```

```

<400> 327
ggtagctttt tttttttttt tttttttttt ttttttttgg tttgaaacag aaattttattc      60
tcanaataat gcacagaagc acagggttgag gctactcttg ggaagcttcc ctcccccttc      120
tcttcctcct ctccctctc tctgaatgcc agggagaaca cagttgaagg aaggaaacat      180
gcaatcacia acaatgaaca actntaaaga caaaaagggt tgggccaaaa gaactcaaca      240
taattaatcc aatgactgtg aanagcttca ctgagtagga ttaanatatt gcagatgtan      300
ngtttncaca ggggtggctnt tcagtgcacc ancggggcct ncttgangga natgaggact      360

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gacncatnCG	ggaaanattct	ttggcctgct	tgetaaactt	ggggntaaag	gcacacnnnc	420
cgggccaccc	gttccactna	nngcctgggg	accanttgct	aatgncnttt	ccnaangntt	480
tttttgntgc	cttgtggttg	nttttggttt	ctggaactgn	tcgncctgnc	ttgnaaacca	540
ttntntaac	nccttaattg	cctttctttt	cnnctgggt	ntgnttccaa	aatnggatta	600
nggggttcang	ngcccctact	tnccgggggc	ngttaaang	naattccncc	nectggngg	658

<210> 328
 <211> 644
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(644)
 <223> n = A,T,C or G

acgcggacgg	tgggtttttg	gcccgtttct	gagcagcgt	tcctttttgt	ccgacatctt	60
gacgaggctg	cggtgtctgc	tgctattctc	cgagcttcgc	aatgccgcct	aaggacgaca	120
agaagaagaa	ggacgctgga	aagtcggcca	agaaagacaa	agaccagtg	aacaaatccg	180
ggggcaaggc	caaaaagaag	aagtgggtcca	aaggcaaatg	tcgggacaag	ctcaataact	240
tagtcttgnt	tgacaaaagt	acctatgata	aactctgtaa	ggaagtcccc	aactataaac	300
ttataacccc	agctgtggnc	tcttgagaga	ctgaagattc	naggctncct	ggccagggca	360
gccctttagg	agcttcttag	ttaaaggactt	atnaactggt	tttnaancac	agacctcaag	420
taattnacac	cagaaatncc	nnggtggaga	atnctccnct	gctggtnnag	angcatgaat	480
aggnncaacc	agctntctct	gncnnaccn	cncttaggnc	naattccgca	ccctgcggcc	540
gttctnatgg	atccnaactn	ggtnccaant	nggcnnacta	tggcatancn	tgccctgggg	600
aantggttcc	nttccaatcc	anaanttcta	tcgnaactta	acgg		644

<210> 329
 <211> 651
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(651)
 <223> n = A,T,C or G

actattagcc	atgggtcaacc	ccaccgtggt	cttcgacatt	gccgtcgacg	gcgagccctt	60
gggcccgcgc	tccttttgagc	tgtttgacaga	caagggtccca	aagacagcag	aaaattttcg	120
tgctctgagc	actggagaga	aaggatttgg	ttataagggg	tcctgctttc	acagaattat	180
tccagggttt	atgtgtcagg	gtggtgactt	cacacgccat	aatggcactg	gtggcaagtc	240
catctatggg	gagaaatttg	aagatgagaa	cttcaccta	aagcatacgg	gtcctggcat	300
cttgtccatg	gcaaatgctg	gacccaacac	aaatgggtcc	cagtttttca	tctgcactgc	360
caagactgag	tggttgatg	gcaagcatgt	ggtgtttggc	aaagtgaata	gaaagggcat	420
gaatattgtg	gaggccatgg	aaccgctttg	ggtccaggaa	tgncnagaac	agcaagaaga	480
acaccattgc	tgactgngga	caactcgaat	aagttggact	tgggggttant	ttaaccacca	540
gaacaattcc	tttgtntnta	aggagancan	ccctcaccca	tttgntngca	tatcctanaa	600
actttgggct	ttcnttngtt	cctttgggtc	aggtttcctg	gtcctccanc	c	651

<210> 330

<211> 643
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(643)
 <223> n = A,T,C or G

<400> 330
 actttntttt tttntntttt tttttttttt ctggaaggnt ctcaggtctt tatttgctnt 60
 ctcaaattcc aggaatngac ttatttaatt aatccatcaa cctctcatag caaatatttg 120
 agaaaacaaa tttatattca gattcttatt ttcagtaggg aagtaagaag ttgcagctca 180
 ttgcacgtaa agttgagaca ganatggaga catccagccc cacctntctg gaacaagaaa 240
 gatgactggg gaggaacac aggtcancat gggaacaggg gttacagtgg acacaagggg 300
 gggctgnctn ttcacctnct tacattatgc taacagggac ncaaaccat tcaggggcct 360
 ttgcnaaaaag aaatgccaaa agctnttgaa gtcncnaagg ggangcgtga anaaaactgc 420
 atttnagtcc ccgggtcctt ngncgggaac ccctnanggn gaaatcncca cactggcggg 480
 ccgtactagn ggatccagct nggncccaat tggnggaata tggnnnaanac tgttcctgtg 540
 ggaaaatggg atccgtccaa ttcnccactt acanncgag cctaaangna aaacntgggg 600
 ngcctatggg gggctacnnn aataatgggt gcctacggcc cnt 643

<210> 331
 <211> 652
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(652)
 <223> n = A,T,C or G

<400> 331
 ggtacagatg gcactgacaa tccccctttt ggtgggggatc agtatcagaa catcacagtg 60
 cacagacatc tgatgctacc agattttgat ttgctggagg acactgaaa caaatccaa 120
 ccagggttctc aacaggctga ctctctggat gcactaatcg tgagcatgga tgtgattcaa 180
 catgaaacaa taggaaagaa gtttgagaag aggcattatg aaatattcac tgacctcagc 240
 agccccgatc agcaaaaagtc agctggatat tataattcat agcttgaaga aatgtgacat 300
 ctccccgcaa ttcttcttgc ctctctcact tggcaaggaa gaaggaagtg gggacagang 360
 agatggccct ttctgcttang tggccatggg ccttnctttt cactaaaagg aattaccgaa 420
 cagcnaaaaag aaagncctta gatagtgaat atggggatga tatctttaga agggngaaga 480
 tgggggtggat gaaattatc attcctgnga agnttgnaaa ctgngcgnct tcnnnaaant 540
 nnnaggcatt centnnctgg centgccatt gccattggnt ccanttgcta tagggatgcc 600
 ccttaaanen ntctcnnna anagtnnaaa acttgc...atn ggatccaacc nn 652

<210> 332
 <211> 648
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(648)

<223> n = A,T,C or G

<400> 332

cgaggtactt	tttttttttt	tttttttttt	tttttttgag	acagagtttc	actcttgctg	60
cccaggctgg	agtgcagtg	cgcgatctcg	gtccactgca	acctcaccct	cccaggatca	120
agcgattctc	ctgcctcagc	cacctgagta	gctgggatta	caggcgccctg	ccactacacc	180
tagccaattt	ttgtattttt	agaagggaca	gcatttcacc	atggtggcca	ggctgggtctc	240
gaactcctga	tctcaggnga	tccaccacc	tcagcctccc	aaagtggngg	gattacaggc	300
gtgagccact	gaaagtcttc	attagttttt	tggttaaatt	ttaaacataa	attatgttat	360
agcaaaaatt	cctaagaatt	gnaaaccact	ttatcagaaa	tatcnnaaat	tcacaaataa	420
tnccaaaatt	tataatagct	tttttcagaa	ctaaaatttt	aaagctactg	anaagnggna	480
aacctnccct	nataggattt	acctaacatt	nnggantaaa	aggnanccan	ngcctgctaa	540
anatccagan	tatctaanaa	tcctnccctg	nntctcnntc	tatnttttca	natccgaatt	600
tttgaaccca	enttangata	nctnntttcc	cccttaacnn	taattccc		648

<210> 333

<211> 656

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(656)

<223> n = A,T,C or G

<400> 333

cgaggtacaa	gatgtccaaa	tattgcgaag	atctatttgg	ggatctcctg	ttgaaacaag	60
cacttgaatc	acatccactt	gaaccaggca	gggcttttgc	atcccccaat	gacctcaaaa	120
gaaaaatact	cataaaaaac	aagcggctga	aacctgaagt	tgaaaaaaac	agctggaagc	180
tttgagaagc	atgatggaag	ctggagaatc	tgctctccca	gcaaaccatct	tagaggacga	240
taatgaagag	gagatcgaaa	gtgctgacca	agaggaggaa	gctcaccctg	aattcaaat	300
tggaaatgaa	ctttctgctg	atgacttggg	tcacaaggaa	gctgttgcaa	atagcgtcaa	360
gaaggcttca	gatgaccttg	aacatgaaaa	caacaaaaag	ggcctggtca	ctgtagaaga	420
tgagcangcg	tggatggcat	cttataaata	tgtaggtgct	ccactaatat	ccatncatat	480
ttgtcaccat	gatcaactac	cccagnctgt	naagggtcaa	ggtttcatgt	ggcanaagaa	540
ccccatattc	ttttacatgg	cttctttaat	gaatcatcgg	cttggtactg	aaaccctgcc	600
attgaattgc	attntacaac	ggcaatgagc	natttcccca	gggaggccng	cnttct	656

<210> 334

<211> 647

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(647)

<223> n = A,T,C or G

<400> 334

acgcgggctg	gaagtgcaga	ggcaaatgca	tttagtgttc	ttcagcatgt	cctcggtgct	60
gggccacatg	tcaagagggg	cagcaacacc	gccagccatc	tgactaggc	tggtggcaag	120
gcaactcagc	agccatttga	tgtttctgca	tttaatgcca	gttactcaga	ttctggactc	180
tttgggattt	atactatctc	ccaggccaca	gctgctggag	atgttatcaa	ggctgcctat	240

```

aatcaagtaa aaacaatagc tcaaggaaac ctttccaaca cagatgtcaa gctgccaaaga 300
acaagctgaa agctggatac ctaatgtcaa tggagtcttc tgagtgnntc ctggaagaaa 360
gtcgggtccc aagctctaag tgctggntct tacatgccac cattcacaag tctttaacag 420
aatgattcan tggctaatac tgatatcata aatgcgnaaa naaagtttgg ttctggcnag 480
aagtcaatgg cancaagtgg naaatttggg acatacncnt ttgtgataag tggaaatactg 540
gngcncnctt acngganana cttaacgtnn tttaanccaa acacaaccct tgaaagnnna 600
agctctaaan accattggct tttttcnggg ngnaaaaaaag gcttaag 647

```

```

<210> 335
<211> 657
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(657)
<223> n = A,T,C or G

```

```

<400> 335
acaggtcaga gtcttctttt cttttctttt tgagatggag ttttgctctg ttgccagact 60
ggagtgcagt ggtgcgatct yggctcactg caatctccac ctcccgggtt caagcgattc 120
tcttgctca gctcccag taactgggac tacaggtgcg cggccaccaag cccagctcat 180
ttttgtattt ttagtagaga tggggtttca cgatgttggc taggatggc tcgatctctg 240
gtcagagtct tttctgtaa tatccttggg aaagaagcaa ttttagactg tagctgttgc 300
aatgcttta aggaagaagc aaaacaactg tcaagtcttc ctgaaatgaa gaaactacac 360
cagggctgct atatcagagc aaccccaacc agcacttcaa tcatgatgcc nacagtggcc 420
cagctgagag accnggagaa agttccagat gcanagactg ngatgctctt gactatggaa 480
atattgcggc cagtaccaag ttagagacca aacaggcata ngnncccgta ttaattggcg 540
tgaattttgc gataaganaa cttggggggg tgctgcggat nccatgatcn ccagaaaact 600
tnngggatgg ggtanaggcc catggcagaa aggttanggt ctttccaaag naaaana 657

```

```

<210> 336
<211> 649
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(649)
<223> n = A,T,C or G

```

```

<400> 336
ggtacgcggg caactatgga attccacagc gtgctctgcg gggtcactcc cactttgtta 60
gtgatgtggg tatctcctca gttggccagt ttgccctctc aggtcctcgg gatggaaccc 120
tgcgctctg ggtctcaca acgggcacca ccacgaggcg atttgtgggc cataccaagg 180
atgtgctgag tgtggccttc tctctgaca accggcagat tgtctctgga tctcgagata 240
aaaccatcaa gctatggaat accctgggtg tgtgcaaata cactgtcagg atgaaaacca 300
cttaaatgg gtgcttngn ncccttntng cccaacagca acaaccctat tatcgtcttc 360
tngggctggg aaaaactggn taaaggatgg aacctggcta actgnaagct gaaaaacaac 420
cacattgggc acacangcta tntgaacacc gngactggct ttttcagang gatcctntgn 480
gcttntggag gcaaggatgg gcaagccatg ttatnggaac tcnaccaang caacaccttt 540
cacctttaan ggggggacat tatnaacgcc ttgggttaac cttaacgtnn ttggtttngn 600
ctgcncaggc ccacattaaa aatgggattt aanggaaaana catttnann 649

```

<210> 337
 <211> 652
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(652)
 <223> n = A,T,C or G

<400> 337
 actcttggtt tgtcaatggg actttccagc aatccaccca agagctcttt atccccaaca 60
 tcaactgtgaa taata_ gga tccataacgt gccaaagccca taactcagac actggcctca 120
 ataggaccac agtcacgacg atcacagtct atgcagagcc acccaaacc ttcataacca 180
 gcaacaactc caaccccggtg gaggatgagg atgctgtagc cttaacctgt gaacctgaga 240
 ttcagaacac aacctacctg tgggtgggtaa ataatacaaga gccttccggt cagtcccagg 300
 ctgcagctgt caatgacaca ggacctnac tctactcagt gtcacaagga atgatgnaag 360
 gacctatga atgtggaatc cagaacgaat taaagcggtg accacagcga ccangcatcc 420
 tgaatgcctt tttggggccan acgacccac cattttcccc tcataccact attaccgtcc 480
 aggggtgnac cttagncttt tcttgccatg cagcctttac ccaccttgac agnattcctg 540
 gctggatgtt gggaacatna gnacncacnc aagagctntt ttttccaaca tnatgggaaa 600
 acannnnct tatactgcag gccattactt ngcctntgcc cagnnggctn cg 652

<210> 338
 <211> 651
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(651)
 <223> n = A,T,C or G

<400> 338
 ggtacatttg aacacacggc tgtgttaaag atgctgctaa tgtcagtcac tgggtgcact 60
 aaaggatctc ttatttttatg taaaacgttg ggattgacaa gatagatctg acactctgtt 120
 aagttaccct ctgaagctac ttcttg gaa atactaatga cagcatcatc ctgccaagcg 180
 aaagaggcag gcataagcaa ggacaaatta aaagggggta agagccttat catgatgagg 240
 agtcttgntt tgacatcttg ggaaaagctg ccatagtgtg aaagtcgtca atttctcacc 300
 atggtttgca gtttgactgn ctctagttag ggtgaagtct ctgagtggca cacaccttaa 360
 gcctgaaggn tttcccttta aattttcatt gagttggccc tcttcagcat atanggcttt 420
 aagaacagaa canaccttg ttttaagtgg gtccatggga taaaatggga atggangact 480
 ngaagaattc aagggtctgg ccactctngca gtattctgaa tatcgaaaat ncnccaaggc 540
 tgctatataa anccccctgg gcaanacttc aatcggaanc ccacggnggc ccnactnana 600
 gncaggaccn ttccaantgg aacatnngan tggggccttt gaggcnnngn n 651

<210> 339
 <211> 634
 <212> DNA
 <213> Homo sapiens

<220>

<221> misc_feature
 <222> (1)...(634)
 <223> n = A,T,C or G

<400> 339
 actttttttt tttttttttt ttttttctag tttcagttat ttattgattt aatcattgta 60
 atctccaata gagattacaa tagagatctc caacatgatt tcatgcattt agaggagaaa 120
 tatttctctgg ttaagtggaa aattgtgcgg atgtggcttc tggaanacct tcattctaaa 180
 gcagcgttat agtgaacat ttcatttana aatctggacg ttccttcttc agcttgctgt 240
 aatccacatt cactgagtag aacttgattt gatcattggg acccagtttg ttccagggct 300
 ctgggttatt tctgcccac aaacatctgg attgaacaat gccagacgca agagatcagt 360
 gttgctccag tagtccagt tccaataaat acnaagagg ggatcaaagc tcggatgctt 420
 cttggcctga ccgatgatct ggcgancat gtttgcnnga aagtctccga ctggaaagga 480
 ganaaccgcc taccccaagc cctaagctaa aaattatntg ccccgcgacc ttggncngna 540
 cccnctaagg caattccacc actggcgcc gtctaangga tccacttggg ccaacttgng 600
 naacatggca nactggtcct ggggaangta tccc 634

<210> 340
 <211> 655
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(655)
 <223> n = A,T,C or G

<400> 340
 ggtactcttc cactcaggtt tccgtgcggc cactccagca cacgcagtat gagcgcttca 60
 tccctcggc ctaccctac tacgccagcg ccttctccat gatgctggg ctcttcatct 120
 tcagcatcgt cttcttgac atgaaggaga aggagaagtc cgactgagg gctagagccc 180
 tctccgcaca gcgtggagac ggggcagga ggggggttat taggattggg ggttttgttt 240
 tgctttgttt aaagccgtgg gaaaatggca caactttacc tctgtgggag atgcaacact 300
 gagagccaag ggggtggagt tgagataatt tttatataaa agaagtttt ccaacttgaa 360
 ttgctaaaag tggnttttt cctatgtgca gtcactctc tcatttctaa aatagggacg 420
 tggccaggca ccgtggctca tgctgtaat ccacactttt ggaggnnng caagcggtta 480
 cgaagtcagg agatcgagac tattctggtt acacgnaaaa cctgncttac taaaagtacc 540
 tgcccggccg gccgntcaa ggcgaatcca cacactggcg ggcgtactan tggatnccaa 600
 cttggaccaa cttgngnaa tatggcatac tggttcctgg nggaaatggt accnn 655

<210> 341
 <211> 648
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(648)
 <223> n = A,T,C or G

<400> 341
 acgaacctac agttttaact gtggatattg ttacgtagcc taaggctcct gttttgcaca 60
 gccaaattta aaactgttgg aatggatttt tctttaactg ccgtaattta actttctggg 120

```

ttgcctttgt ttttggcgtg gctgacttac atcatgtgtt ggggaagggc ctgcccagtt      180
gcactcaggt gacatcctcc agatagtgtg gctgaggagg cacctacact cacctgcact      240
aacagagtgg ccgtcctaac ctcgggcctg ctgcgagagac gtccatcacg ttagctgtcc      300
cacatcacia gactatgcca ttggggtaag ttgtgtttca acggaagtg ctgtcttaaa      360
ctaaatgtgc aatagaaggn gatgggtgcca tcctaccgnc ttttcctggt tcctanctgn      420
gtgaatacct gctacgtcaa atgcntacca ggttcattct nccttnnact aaaacacaca      480
ggtgcaacag acttgaatgc taagtatacc taattggata tgggatttaa ttttctttct      540
tacaancatt tgtattgcta acaggccaaa atttcagtta cccttagggg gggttaacaat      600
cnaattaaac ctgggaggca tacnttgntc aaatattact gnaaaaaa      648

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<210> 342
<211> 342
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1) ... (342)
<223> n = A,T,C or G

```

```

<400> 342
ggtaacttttt tttttttttt tttttttttt gttttttttt tttttttttt tttttttttt      60
tggctntana ggggggtanag ggggtgctat agggtaaata cgggccctat ttcaaanatt      120
tttaggggaa ttaattctag gacnatgggc atgaaactgn ggtttgctcc acanatttca      180
nagcattgac cgtagtatac ccccggtcgt gtancggtga aagtggtttg gtttaaacgt      240
ccgggaattg catctgtttt taagcctaata gtggggacag ctnatgagtg caaacgtct      300
tgngatgtaa ttattatacc aatgggggct ttaatcggga at      342

```

```

<210> 343
<211> 484
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1) ... (484)
<223> n = A,T,C or G

```

```

<400> 343
ggtacgatgc ctagtgatga gtttgctaata acaatgccag tcaggccacc tacggtgaaa      60
agaaagatga atcctagggc tcagagcact gcagcagatc atttcatatt gcttccgtgg      120
agtgtggcga gtcagctaaa tactttgacg ccggtgggga tagcgatgat tatggtagcg      180
gaggtgaaat atgctcgtgt gtctacgtct attcctactg taaatatatg gtgtgctcac      240
acgataaacc ctagggaagcc aa'tgatata atagctcaga ccatacctat gtatccaaat      300
ggttcttttt ttccggagta gtaagttaca atatgggaga ttattccgaa cctggttagga      360
taagaatata aacttcaggg tgaccgaaaa atcagaatan gtgttggtat agaatggggg      420
cttcttcttc ngcgggggctn aanaaggtgg tggtncgcg tcctggccng gcnggcgctc      480
gaan

```

```

<210> 344
<211> 657
<212> DNA
<213> Homo sapiens

```


<220>
 <221> misc_feature
 <222> (1)...(657)
 <223> n = A,T,C or G

<400> 344
 cgaggtacgc gggattgttc tggggcttgt cctcctttct gttacgggcc agggcaaggt 60
 ctttgaaagg tgtgagttgg ccagaactct gaaaagattg ggaatggatg gctacagggg 120
 aatcagccta gcaaactgga tgtgtttggc caaatgggag agtgggttaca acacacgagc 180
 tacaaactac aatgctggag acagaagcac tgattatggg atatttcaga tcaatagccg 240
 ctactgggtgt aatgatggca aaaccccagg agcagttaat gcctgtcatt tatcctgcag 300
 tgctttgctg caagataaca tcgctgatgc tgtagcttgt gcaaaaangg ttgtcccgtg 360
 atccacaagg cattaagagc atgggtggca tggagaaatc gttgtcaaaa cagagatgtc 420
 cgcagtatgt tcaanggtgt ggagtgtaac tncagaattt tccntcttca ctcatattggc 480
 tctctacatt aaggagtagg aaataantga aagggtccct ccattaattt ccttcaaca 540
 aataattttt tccgaaacng gaccaaatat ggccttcttn tagannataa tgtcntaagg 600
 ggnattttatt ttaagcnnca canttttaat ttgcaaanaa ctatctgggg aaaatac 657

<210> 345
 <211> 662
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(662)
 <223> n = A,T,C or G

<400> 345
 ggtacgcggg cgactcttag cgggtggatca ctcggctcgt gcgtcgatga agaacgcagc 60
 tagctgcgag aattaatgtg aattgcagga cacattgatc atcgacactt cgaacgcact 120
 tgcngccccg gggttcctccc ggggctacgc ctgtctgagc gtctcttgca aaaaaaaaaat 180
 aaannanaaa acancaaagta caatttaatg cntanaaagg cctctctcca taaaactcan 240
 cncctttacag atgtangaat atataagcnn tgccaaaatt actaatntgc cacatacnaa 300
 gcatcaattc cagggtgctag tnagnnggaa aaaaanttgg agaattcggc cctcgangag 360
 ctccanant taanctnctt tactaantnc canggttctt tcaagcatgg aaaaattaat 420
 ngtgctncat ngatnaangn cttgtcattg ggccttnttt cctngacctg gcccggccgn 480
 ccgttcnaaa ggctaaatcc agacactgcg gccgttntaa tggttcnac ttgggccaag 540
 cttgggnaat catgggcaaa gctgttcctg ggnaaatnt tatccnctcc aattcncaca 600
 natakgaanc tgaancttaa gtgnanntn gggngctaaa agtggcnaa ctcctttnat 660
 gg 662

<210> 346
 <211> 654
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(654)
 <223> n = A,T,C or G

```

<400> 346
acttcttggc cgcctcacta gcactctcgg cctgcttttt aaaggcttca ttggaggcca      60
gcagcgtggc ctgctgcgaa atgagagtca ccaggcctct aagcaggaag gacagcagcg      120
aggaaaagcc agcaatgtag agattcctct gggcacggaa aagcttcatg tggagagtgt      180
ccatggcccc gggattgttc tggagggttc ccttttcggt cacatcatca tacttccgaa      240
tttcgcgcac ggcacatgat accaacagca caaggatgac aatgagaacc acaaagaagg      300
tggtgccata ggacactaac aactccacca gccgggactt gaaaatcttc tgccatcttt      360
taggagaaat gaagggaatg cagagaagca acacaacaaa gaccttcgca tagaggaagg      420
tggcaactgc agtccactgc agactcatcc tgggtgctana agggttccac aggaagatgt      480
gaacttgtnn cgagttttcca cagtcaacgt gtcccccgta ccttnggcng ngaacacnct      540
taaggcgaat tccaccactg cnggccgtct antggatcca actnggncca acttggcgaa      600
tatggcaaat tgttctnggg naaatggttc ngtcaattcc ccantacnac cgggaa      654

```

<210> 347

<211> 536

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(536)

<223> n = A,T,C or G

```

<400> 347
ggtactaatt taaggtaaca attctcgagg taaaataaagg cattatagta acacaatttt      60
catgcctcag caattaacaa tgattttcgt ttaattctct tccaactcta cagacataat      120
tctgctttca ccttcatcac gctttcatat ggttttaaca ggggatacac ctctctctct      180
aagaatctct gcacctgctg ggaggcacga ccagtgaag aagaaggatc cagtaaatga      240
tccaactggg agtgaatggg actgaagtag gcacaaacct ggatacgctc tatgaggncn      300
ttgcaccccc ttctgcttta accacagaag ctgacctgctg agaaagcact ctgattttct      360
catggcaatc ctggcggtta ccttcacttt gaccatggcc atgatgatgg tctctgtggc      420
catgaaangc agctcttgcc gaatgcgccg tcaattactt tggggtacct gccnnggccg      480
gccgntcnaa nggcgaattt cagccactgg cngncgtact agnggatcca actcgg      536

```

<210> 348

<211> 665

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(665)

<223> n = A,T,C or G

```

<400> 348
ggtacgcggg gagtgcggct aggccttagg tgggttcgtg cgccttctac ctgctgttt      60
cggttttctt ggctcctcgg cccttttctc cctgtttgca gctgggagcg gacgaagcgc      120
gaagctggga ttttttactg tctcctgaag aatttaacac aaacatggat atcagaccaa      180
atcatacaat ttatatcaac aatatgaatg acaaaattaa aaaggaagaa ttgaagagat      240
ccctatatgc cctgttttct cagtttggtc atgtggtgga cattgtggct ttaaagacca      300
tgaagatgag ggggcaggcc tttgtcatat ttaaggaact gggctcatcc acaaatgcct      360
tgagacagct accaggattt ccattttatg gtaaaccaat gccaatacag tatgcaaaaa      420
cagattcggg tataatatca aaaatgcgtg gaacttttgc ttaaaaaaaaa aaannnnnna      480

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naaaaaagtc ctgccnggcc gcccggtcaa anggcgaatt naccactggc ggccggttcta 540
gnggatccaa ctnggnacca acttggcgta atatggcaaa actggtncgc ngngaaatgg 600
tatccgttan aattcccaca cttcaaccgg aacctnaang taaacctggg gcctaagagn 660
gacnn 665

```

<210> 349

<211> 474

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(474)

<223> n = A,T,C or G

<400> 349

```

acttcgtcag tttgtaagac atgagtcgga aacaactacc agtttgggttc ttgaaagatc 60
cctgaatcgt gtgcacttac ttgggcgagt gggtcaggac cctgtcttga gacagggtgga 120
aggaaaaaat ccagtcacaa tattttctct agcaactaat gagatgtggc gatcagggga 180
tagtgaagtt taccaactgg gtgatgtcag tcaaaagaca acatggcaca gaatatcagt 240
attccggcca ggcctnagag acgtggcata tcaatatgtg aaaaaggggt ctccaattta 300
tttgaaggga aaaatagact atggtgaata catggataaa aataatgtga ggcgacaagc 360
ncaaccatca tagcttgatn atattatatt tctgagtgcc agaccaaaga gaaggagtnt 420
aaanggatga tcntcttttg ggcattcatt tgggacctn ggccgggaac accc 474

```

<210> 350

<211> 452

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(452)

<223> n = A,T,C or G

<400> 350

```

acgcggggac cgtggagagc agagcgcggc ggctggaagc tgctaagtca gagccgcgat 60
gttccggatt gagggcctcg cgccgaagct ggacccggag gagatgaaac ggaagatgca 120
cgaggatgtg atctcctcca tacggaactt tctcatctac gtggccctcc tgcgagtcac 180
tccatttatc ttaaagaaat tggacagcat atgaagacag gacatcacat atgaatgcac 240
gatatgaaga gcctgggttac agtttcgact cctctctgca agtgaatagg cccagaaagg 300
tgtaagagac tctttgaatg gacataaaat tctgcttggt aagaacaagt ttggctctgg 360
taactgacct tcaaagctaa aatataaaac tatttgggaa agtatgaaac gatgtcttcg 420
tgatctggtg taccttggnc gngacacgc tt 452

```

<210> 351

<211> 616

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(616)

<223> n = A,T,C or G

<400> 351

```

ggtacgcggg aataattcca tagtcaagag catcacagtc tctgcatctg gaacttctcc      60
tggtctctca gctggggcca ctgtcggcat catgattgga gtgctggttg gggttgctct      120
gatatagcag ccttgggtga gtttcttcat ttcaggaaga ctgacagttg ttttgcttct      180
tccttaaagc atttgcaaca gctacagtct aaaattgctt ctttaccaag gatatttaca      240
gaaaagactc tgaccagaga tgcagaccat cctagccaac atcgtgaaac cccatctcta      300
ctaaaaatac aaaaatgagc tgggcttggt ggcgcgcacc tgtagtccca gttactnggg      360
aggctgaggc aggagaatng cttgaacccg gnaggtggag attgcagtga gccagatcgn      420
acnactgnac tcagtctggc aantgagnag gcttccatct nanaangan aganangan      480
actnlnacct ggacctgccn ggccggtcgt ttgngcaggt cnggagattt attcccttng      540
ggtggggngc nntaattggn tgntgggcn attcangttt tgggaatttc nnttgggnn      600
naaaanggga aattttt

```

<210> 352

<211> 603

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1) ... (603)

<223> n = A,T,C or G

<400> 352

```

ggtacggcac ttggcgtaaa gccgcttccc tcaagagtaa ctacaatctt cccatgcaca      60
agatgattaa tacagatctt agcagaatct tgaaaagccc agagatccaa agagcccttc      120
gagcaccacg caagaagatc catcgcagag tcctaaagaa gaacccactg aaaaacttga      180
gaatcatggt gaagctaaac ccatacgcaa agaccatgcg ccggaacacc attcttcgcc      240
aggccaggaa tcacaagctc cgggtggata aggcagctgc tgcagcagcg gcactacaag      300
ccaaatcaga tgagaaggcg gcggttgca gcaagaagcc tgtggtaggt aagaaaggaa      360
agaaggctgc tgttggtggt aagaagcaga agaagcctct ggtgggaaaa aaggcagcag      420
ctaccaagaa aaccagcccc tgaaaagaac ctgcagagaa gaaacctact acngaggaga      480
agaagcctgc tgcataactc ttaaatgtga atatttcntt aagggcnaat nttttggcag      540
gttctttgga taagaentnt ttcngngtg ggaataaan tnnntattn nnggctntcc      600
tgg

```

<210> 353

<211> 604

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1) ... (604)

<223> n = A,T,C or G

<400> 353

```

ggtaccgact gtttttgaca actatgcagt cacagttatg attggtggag aaccatatac      60
tcttgacttt tttgatactg cagggcaaga ggattatgac agattacgac cgctgagtta      120
tccacaaaca gatgtatttc tagtctgttt ttcagtggtc tctccatctt catttgaaaa      180
cgtgaaaaga aagtgggtgc ctgagataac tcaccactgt ccaaagactc ctttcttgct      240

```

```

tgttgggact caaattgatc tcagagatga cccctctact attgagaaac ttgccaaagaa 300
caaacagaag cctatcactc cagagactgc tgaaaagctg gcccgtgacc tgaaggctgt 360
caagtatgtg gagtgttctg cacttacaca gaaaggccta aagaatgtat ttgacgaagc 420
aatattggct gccctggacc tncagaccga agaagacccc aagtgtgtgc tgctatgaac 480
atctttcaga gcctttcttg nacagctgga ttggcatctt cttaaagcca tgnttaaaatt 540
caacttanga ttaaaattaa aattcgtttt gcannatggc caatgcctgg actaaccan 600
ggcn 604

```

<210> 354
 <211> 631
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(631)
 <223> n = A,T,C or G

```

<400> 354
ggtacttttt tttttttttt tttttttttt tttgggacgg agtcatgctc tgtcgcccag 60
gctggagtgc agtggcatga tctcggtcca ctgcaagctc cgcctcccgg gctcatgcca 120
ttctcctgcc tcagcctccc gagtagctga gattataggg acctaccacc acgcccggct 180
aatttttgta tttttagtag agacgggggt taccatgtt gaccaggctg gtctcgaact 240
cctgacctta ggtgatccac tcgccttcac ctcccaaagt gctgggatta caggcgtgag 300
ccaccgtgcc tggccacgcc caactaattt ttgnattttt agtaagagac agggtttcac 360
catgttggcc aaggctgctc tttgaactcc tgacctcatg taatcgacct gcctttggcc 420
ttccaaaagt gctgggatta ccagggtgtga gcccacaagc cccggnacct ggccnggcng 480
gccgtttaaa agggcgaaat cagcacaatg gnnggccgta ctaaggggat ncnanctttg 540
nanccaactt tgggggaaat atggggcana actggttcct ngngnaaatg gtaaccgtta 600
caaattcccn caaanttttg nnccgggagg n 631

```

<210> 355
 <211> 626
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(626)
 <223> n = A,T,C or G

```

<400> 355
ggtacgatgc ctagtgatga gtttgctaata acaatgccag tcaggccacc tacggtgaaa 60
agaaagatga atcctagggc tcagagcact gcagcagatc atttcatatt gcttccgtgg 120
agtgtggcga gtcagctaaa tactttgacg ccggtgggga tagcgatgat tatggtagcg 180
gaggtgaaat atgctcgtgt gtctacgtct attcctactg taaatatatg gtgtgctcac 240
acgataaacc ctaggaagcc aattgatatc atagctcaga ccatacctat gtatccaaat 300
ggttcttttt ttccggagta gtaagttaca atatgggaga ttattccgaa gcctggtagg 360
ataagaatat aaacttcagg gtgaccngaa aaatcagaat aggtgttttg tttagaatgg 420
ngtcttctnc ttcnctggg gttnnaagaan gtnggggttc nngcgtnctn gntcgggcgg 480
ntggttttta nggcnaaat tcnngnataa ttggcggcng ttactaagng gnatctant 540
tggtnccaaa nttgngnta atcatggtnc tagctngtnc tcngtgntaa attggnntcc 600
tgttaaattn tntnnaatnt tntggc 626

```

<210> 356
 <211> 617
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(617)
 <223> n = A,T,C or G

```

<400> 356
actttttttt tttttttttt ttttttttota gtttcagtta tttattgatt taatcattgt      60
aatctccaat agagattaca atagagatct ccaacatgat ttcattgcatt tagaggagaa      120
atatttcctg gttaagtgga aaattgtgcg gatgtggcct ctggaanacc ttcattctaa      180
agcagcgtaa tagtgaaaca ttccatttan aaatctggac gttccttctt cagcttgctg      240
taatccacat tcaactgagta naacttgat tgatcattgg gaccagttt gttccagggc      300
tctgggttat ttctgtccca acaaacatct ggattgaaca atgccagacg caagagatac      360
agtgttgctc cagtagctcc agttccaata aatacnaaga gggggatcaa gctcggatgc      420
ttcttggcct gaccgatgat ctggccggaa ncatgtttgc cggcaaaagg ctccnacttg      480
ggaaagggga naaccgcct aaccnccagg gctaagctt aaaatttttg gccccgggta      540
ccttggccgg gaccccttaa gggngnaatt ccnnccctt gggggggcgt ttaangggan      600
ccaacttggg ccaaatt

```

<210> 357
 <211> 611
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(611)
 <223> n = A,T,C or G

```

<400> 357
ggtacttttt tttttttttt tttttttttt ttttaggcaa agaactttat taatctttgt      60
ttcaaaacttg attcccaggc ttcttcggct taattagctg caaagaatga attgngtata      120
agcaaaaact gaaaagagct gcagtgtcca aggggcttgg gcttaaaaat attagagatc      180
tagattttat cagatccata acaaaaaatt tcttaaaaag cagtcataat ataaaatagc      240
agctcccagt aacttcttca ggnntttatct tcagaagttg actcaattca gtttgectca      300
ttcttgggaag cctcatcaaa attctccaca agatctggaa cttcatcatc atcatcctct      360
ccagtaacaa gtggngcttt tccatcccca gantggttgg gcanaacttt ngncagctc      420
cttaacttag cagactatc ggaccaagc tnggttnaaa aanctgggaa cnatttntgn      480
naactggttt ggttnaacan ggcntgnaag ggggaaagg gthccctgcc caaaaaaccn      540
ggaccttag ggtgnnaaag gggacctggc cctgggttgg aaccaanten ccttttnana      600
ccnnanaatn g

```

<210> 358
 <211> 619
 <212> DNA
 <213> Homo sapiens

<220>

<221> misc_feature
 <222> (1)...(619)
 <223> n = A,T,C or G

<400> 358
 ggtactttttt tttttttttt tttttttttt ttgagatgga gtctcgctct gtgcgccagg 60
 ctggagtga gtggcgcaat ctctgctcac tgcaacctcc gctcctggg ttcaagcaat 120
 tctcctgtct cagcctccca aatagctggg attacgggca tgtgtcacga cgctcggcta 180
 atttttgtat ttttagtcga gacgaggttc caccatgttg gctaggctgg tctcaaactc 240
 ctgacctcag gtgatccgcc tgctcggcc tcccaaagtg ttaggattac ggggtgtgagc 300
 cactgcgccc agcaagcaac ctagatttta aaacaacatg agataaataa gcctaattgg 360
 atttaactac atctaacatt tttactaata gttgnaatac tggtagaatt tggaaactat 420
 tatatatatt atgcngaaaa gtaaataatt ctggtaaat canttanggn cntgaattt 480
 nagcataggg gaaaaaaaga tgccntttta aatccaataa gtaaaaaccn tttaaccctn 540
 tntttaaatt ggaantttcc cccaatttnt tattaatttc aacttntttt gaaaactcat 600
 ntctcnaaa antnggggg 619

<210> 359
 <211> 624
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(624)
 <223> n = A,T,C or G

<400> 359
 ggactttttt tttttttttt tttttttttt ttttttgagg gaaaaccgg taatgatgtc 60
 ggggttgagg gataggagga gaatggggga taggtgtatg aacatgaggg tgctttctcg 120
 tgtgaatgag ggttttatgt tgttaatgtg gtgggtgagt gagccccatt gtgttggtgt 180
 aaatatgtag agggagtata gggctgtgac tagtatgttg agtcctgtaa gtagganagt 240
 gatattgat caggagaacg tggttactag cacagagagt tctcccagta ggttaatagt 300
 ggggggtaag gcgaggttag cgaggcttgt tanaagtcac caaaaagcta ttagtggggag 360
 tagagtttga agtccttgag agaggattat gatgccactg ngaatgcntt cctaatttga 420
 gtttgctagg cagaatagtn atgaggatgt aaacccctng gccaattatt aaaaatgact 480
 gcncccgtag aacttnaggg ggtttggatt aaaaangctt gtacttccaa nggctntntg 540
 gctnatttta aaaaatttcc ctnnncnaat ttagggcttn ttnnncnaag ccnanagggn 600
 cccnancct ttcccggggg ggc 624

<210> 360
 <211> 611
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(611)
 <223> n = A,T,C or G

<400> 360
 acgcggggag gcggaggctt ggggtgcgttc aagattcaac ttcacccgta acccaccgcc 60
 atggccgagg aaggcattgc tgctggagggt gtaatggacg ttaatactgc ttacaagag 120

```

gtttctgaaga ctgtcctcat ccacgatggc ctagcacgtg gaattcgcca agctgccaaa 180
gccttagaca agcgccaagc ccattctttgt gtgcttgcat ccaactgtga tgagcctatg 240
tatgtcaagt tgggtggaggc cctttgtgct gaacacccaaa tcaacctaat taaggttgat 300
gacaacaaga aactaggaga atgggtaggc ctttgtaaaa ttgacagaga ggggaaaccc 360
cgtaaagtgg ttggttgtag ttgtgtagta attaanagct atggcaagga gtctcagcca 420
aggatgtcat tgaagagtat ttcaaagtcc agaaatgaag aaattaaatc nttggcttac 480
ttaaaaaaaaa annnnnnnnnn aaaaaaaagg tccttggggc gnacaccctt aaggggnaat 540
tcnnnnccctt gggggccntt ataangggnn ccnacttggg ccaaattggg naaananggg 600
naaanttttt n 611

```

```

<210> 361
<211> 404
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(404)
<223> n = A,T,C or G

```

```

<400> 361
acatatTTTA atagaaagat acaacctttt tatttttact cctttttattt ctgctgcttg 60
gcacattttt gagttttccc acattatttg tctccatgat accactcaag cagtgtgctg 120
gacctaaaat actgacttta gttagtatcc ttggattttt agattcccag tgtctaattc 180
cctgttataa tttgcgcaaa caaaacaaaa tgttatgata atctttctcc actgttctaa 240
tatatattgt atttttattt gatagcttgg gattttaaac atctctgttg aaggcttttg 300
atccttttga gaaataaaga tctgaaagaa atggcataat cttaaaactt gataaaaaaa 360
aaanannnnn nnnaaaaaaa aaagtacctn ggccngnacc acgc 404

```

```

<210> 362
<211> 322
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(322)
<223> n = A,T,C or G

```

```

<400> 362
gggtactttt tttttttttt tttttttttt ttttttggag ttgtaggcaa atgtttaatt 60
aattctgctc atatgcacat ctgaaagcat gagacacact ccacagacag cacgcactgg 120
ggctgggtgg gcanatgggc actcgccgat taggtattaa tgtcaataat acgtgcataa 180
agtgtgata aaataactta agtggtacaa aaagagacag tccacggtgg ctgcaggcac 240
atgcaggcgg gactgggtca gacactccag ggctgcacat gttccagctg gcctgagtcc 300
gacacgtcat agctggcctt gt 322

```

```

<210> 363
<211> 616
<212> DNA
<213> Homo sapiens

```

```

<220>

```


<221> misc_feature
 <222> (1)...(616)
 <223> n = A,T,C or G

<400> 363
 cgaggtacgc gggctaagca agggaaaaat aacagtttct ctgagccaga gaagacttga 60
 tcacagttct ccaagcatcg tgatagcaat gcttaacccc aggaagattt caaggcaggg 120
 agaagaacat ttcaataaag attcttggtta acccatttat gcctagtgtt ccattattgg 180
 aatgctaagc ttgtgggagt catttacatc ctactgctca aagtcattgc caaggctctga 240
 tttttcacac aaaaaattgc aacccccagc ataaatgttt agctactgtc atcagtttagc 300
 aaattcatcc acacaaacac aattagagtt tgggtttttt ttaagctttt caaaacttac 360
 taaactggca caattttata tgtatgctat ttggtgnatt tatgcttaag agcnaaaaaag 420
 tttgatggga ttttaaattc angccaagcc tacacgctga gacaatccct acaaccatgg 480
 nagtaactaa ngaaccttta tctaagnttt taagttttta anggagngct taatggttca 540
 ngctangtt ggaatttcct tcanaaattt cntcttttaa aaaattttcc caaaatnggt 600
 ccttaaaaaa ctcann 616

<210> 364
 <211> 618
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(618)
 <223> n = A,T,C or G

<400> 364
 cgaggtacgc ggggtcttct gcctaacgcc gccaacatgg tgttcaggcg ctctcgtggag 60
 gttggccggg tggcctatgt ctccctttgga cctcatgccg gaaaattggt cgcgattgta 120
 gatgttattg atcagaacag ggctttgggc gatggacctt aactcaagt gaggagacag 180
 gccatgcctt tcaaatgcat gcagctcact gatttcatcc tcaagtttcc gcacagtgcc 240
 caccagaagt atgtccgaca agcctggcag aaggcagaca tcaatacaaa atgggcagcc 300
 acacgatggg ccaagaagat tgaagccaga gaaaggaaag ccaagatgac agattttgat 360
 cgttttaaag ttatgaaggc aaagaaaatg aggaacagaa taatcaagaa tgaaagttaa 420
 agaaacttca aaaggcagct nttctgaaag cttnttccca aaaaagcacc tgggtacctg 480
 gccgggcccg ccgttttaaaa gggcnaattc caccactggc ggccgtctan ngggatccaa 540
 cttnggacca acttgngnga atatggcnaa attgttctct gggnaaatgt ttncgttcaa 600
 attncncaaa ttacggcc 618

<210> 365
 <211> 601
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(601)
 <223> n = A,T,C or G

<400> 365
 acgtcctgga ggactctatt gtggaccac agaatcagac catgactacc ttcacctgga 60
 acatcaacca cgccgggctg atgggtgggtg aggaacgatg tgtttactgt gtgaactctg 120

```

acaacagtgg ctggactgaa atccgccggg aagcctgggt ctctcttagc ttatttggtg 180
tctccagagc tgtccaggaa tttgggtctt cccggttcaa aagcaacgtg accaagacta 240
tgaagggttt tgaatatatc ttggctaagc tgcaaggcga ggccccttcc aaaacacttg 300
ttgagacagc caaggaagcc aaggagaagg caaaggagac ggcaactggc gctacagaga 360
agccaaggac ctgccagca aggcggccac caagaacagc agcagcagca acagtttgtg 420
taaccagnct accaacaaca nagnaccca nacaggtagg cttacccctt tggcctcctt 480
taatggacct tggccgggaa cacccttang gcgaattcag nactggggg ccgtactang 540
ggatccnctt ggaccaactt ggggaaacag ggcaaaattg ttcttgggga aattntatcc 600
n 601

```

```

<210> 366
<211> 321
<212> DNA
<213> Homo sapiens

```

```

<400> 366
actttttttt tttttttttt tttttttgag atggagtctc actctgtcgc ccaggctgga 60
atgcagtggg gcaatctcag ctactgcaa cttccacctc ccagggtcaa gtgattctcc 120
tgcctcagcc tccacatat ctgggactac aggtgcacac caccatgcc agctaatttc 180
tttgtatttt ttagtagaga cgggggttca tcttattggg caggctgggc tcgaactcct 240
aaccttgtag tctgccacc tcggccttcc aaagtgtcgg gattacaggc gtgagccacc 300
gtgctcggcc accgcgtac c 321

```

```

<210> 367
<211> 264
<212> DNA
<213> Homo sapiens

```

```

<400> 367
actgatcatg gagttaatca acaatgtcgc caaagcccat ggtgggttact ctgtgtttgc 60
tggtgttggg gagaggaccc gtgaaggcaa tgatttatac catgaaatga ttgaatctgg 120
tggtatcaac ttaaaagatg ccacctctaa ggtagcgtg gtatatgggc aaatgaatga 180
accacctggg gctcgtgcc ggtagctct gactgggctg actgtggctg aatacttcag 240
agaccaagaa ggtcaagatg tacc 264

```

```

<210> 368
<211> 488
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc feature
<222> (1)..(488)
<223> n = A,T,C or G

```

```

<400> 368
ggtacagatg cacaggaggg catagggttt aggcanaagg gagcacaan gttgaagatg 60
aggcgctgcc atcaatgctg ggacttcagg cnaagggcag gaactgagga agccacaagg 120
gaggacattt tctgcagttg ctgaancagt ancaactagg tcctgagaaa gccctntctc 180
gtggaagaat aacagccagg cnggaaagct tttcatcctg caaagctggg gaagaagatt 240
cttccttaaa ttgtcatctg cacttcagct cangaatcct gttggctgaa gtccagagtg 300
tccttttctg attcctgaag tanatnaaca gcccnngccc aangaagagn aggnntagta 360
caaagccnnc tncgcgtacc tgtncgggcg gnngttcgna aggnntcaaat tccagcacia 420

```

ttgnctgccg ttantagttg gattctnact ttngtactta ncttggcgta ntttatggtn 480
ataanttg 488

<210> 369
<211> 602
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(602)
<223> n = A,T,C or G

<400> 369
acgggggttt cactacttct cccccggact ccttggtagt ctgttagtgg gagatccttg 60
ttgccgtccc ttgcctcct tcaccgccgc agacccttc aagttctagt catgcgtgag 120
tgcattctcca tccacgttgg ccaggctggt gtccagattg gcaatgcctg ctgggagctc 180
tactgcctgg aacacggcat ccagcccgat ggccagatgc caagtgacaa gaccattggg 240
ggaggagatg attccttcaa caccttcttc agtgaaacgg gtgctggcaa gcatgtgcc 300
cgggcagtgt ttgtagactt ggaaccacaa gtcattgatg aagttcgcac tggcacttac 360
cggcagctct tcaccctgag caactcatca caggcnagga aaaatgctgc aataactatc 420
ccgaaggcac tacaccattg gcaaggagaa taattgacct gtgttgacc gaattcgcaa 480
gctggctgac catgcaccgg cttaagggtt nttggttttc ccaacttttg gggggggaac 540
tgggtttngg gtaaccctnn tggtnatngg aacgntttta antggatttt gggaanaaan 600
cc 602

<210> 370
<211> 257
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(257)
<223> n = A,T,C or G

<400> 370
actttttttt tttttttttt ttttagttttt ttttattttt taaaaatata ctggagaatc 60
atgcaatgct gccagcattg gatgcaatcc gggggccacaa gtctgcacac tcctttgcta 120
ctggctcctgt aatggcagaa cctttcatct cgcctttatt gntcactatg actcctgcat 180
tatcttcaaa ataaagaaac acgcatctt ttctacggta tgactttcgt tgtcgaatga 240
ccactgctgg atgtacc 257

<210> 371
<211> 607
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(607)
<223> n = A,T,C or G

```

<400> 371
acttttttttt tttttttttt tttttttgct atttagtttt tatttcataa tcataaactt      60
aactctgcaa tccagctagg catgggaggg aacaaggaaa acatggaacc caaaggggaa      120
tgcagcgaga gcacaaagat tctaggatac tgcgagcaaa tggggtggag ggggtgctct      180
ctgagctaca gaaggaatga tctggtggtt aagataaaaac acaagtcaaa cttattcgag      240
ttgtccacag tcagcaatgg tgatcttctt gctggctcttg ccattcctgg acccaaagcg      300
ctccatggcc tccacaatat tcatgccttc tttcactttg ccaaacacca catgcttgcc      360
atccaaccac tcagtcttgg caagtgcaga tgaaaaactg ggaaccantt ggggttgggt      420
ccacatttgc catggacaag aatgccagga acccgatatgc ttaaggatg aagtctcatc      480
ttcaaaattc ttccccataa atggacttgc caccagngcc attatggcgt gtgaagtccc      540
cancctggcc cataaacctt ggaaaaatnt tggnaaaccc gaaccctttt aaccaatcct      600
ttttttc                                         607

```

<210> 372

<211> 607

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(607)

<223> n = A,T,C or G

```

<400> 372
acgaatgtgg gaattactca ggagcagcag aatatcttta tttttttaga gtgctggttc      60
cagcaacaga tagaaatgct ttaagttcac tctggggaaa gctggcctct gaaatcttaa      120
tgcagaattg ggatgcagcc atggaagacc ttacacgggtt aaaagagacc atagataata      180
attctgtgag ttctccactt cagtctcttc agcagagaac atggctcatt cactggctct      240
tgtttgtttt cttcaatcac cccaaaggtc gcgataatat tattgacctc ttctttatc      300
agccacaata tcttaatgca attcagacaa tgtgtccaca cattcttcgc tatttgacta      360
cagcagtcac aacaaacaag gatgttcgaa aacgtcggca ggttctaaaa agatctagg      420
taaaggttat tcaacangga gtcttacnca tntaagacc cttacngga atttggtgaa      480
tggttatatg taactttgac ttttaangggc tcaaaaaaag ctnaggggat gtgaatcaag      540
cttgngaagg ctttttttgg gggctngntt nngggttnt tgnaaagncc ngttttnttt      600
ttggaat                                         607

```

<210> 373

<211> 618

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(618)

<223> n = A,T,C or G

```

<400> 373
acttttaatg tttgctgttc aaacgaaaat agattggatc ttggttaagt tcacttggtt      60
tggccaggca cagtggctca cgctgcagt cccagcactt ggggaggtgg aggcggggccg      120
atcacctgag gtcaagagtt tgagaccagc ctggctaacg cgggtgaaacc ccatttctac      180
taaaaataca aaaaattagc tgggcgtggg ggtgcgcgct tgtaatccca gctactcggg      240
aggctgagcg aggagaatcg cttgagccag agaggcaaag gttgcaataa gccaatagat      300
cgccattgta ttccagcttg gacaacaaga gcgaaactct gtctaaaaaa aaaaaaaaaa      360

```

```

cacacacaca acacaatatt ttcacgcctg taaacctagc acattgggaa gccaaagggtg 420
gaggattgct tgaggccagg agttcaaggc ttgcantgag ctatgaatgn acactgnacc 480
tttggncgng aacacnctta nggccaaatt ccngcacact tggggggccg tactaanggg 540
atcccanctt tggnnccaaa nttggngnaa acatggggcaa aattggtnc tggngaaaat 600
ggttccgttc caaatccc                                     618

```

```

<210> 374
<211> 605
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(605)
<223> n = A,T,C or G

```

```

<400> 374
accagctgc tgcccacatt tctggtccag agtcccgaac cccgagcact gggatgcctg 60
gctactccga gcgttatcca gactagcgag tgggaggcag atgtaaaatc tggaacgcag 120
attttagttt gttggaagga gaaatgtaac atagtgaacc acgcattctt ggagggtgta 180
aagcagagac agccaagagc caaggcactg atgtttgaac tggaaaactc aaaacgttta 240
ataagagtct tcaggatggg tttgaactag acaagctaga aatttcttta gaacaccagc 300
tctagcatgc atctcccact tttggctttc ctggagagga gcttgaagag gtggttctgc 360
agacagccac agtgatactc aggaaaacna gaggaatgga tttgactttt ctgctaggaa 420
tctttggtat aagttctcct tgagttgtaa gangcatgga aatatacatg aaactgaana 480
acctgcaagg aanggaatg ggaacntttc atctgagtgn aaactaacca agtnggcaat 540
ttngacttga aacccttgaa accttcnagt ccaantcctg gtttggggga taaangaacc 600
ggncn                                     605

```

```

<210> 375
<211> 602
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(602)
<223> n = A,T,C or G

```

```

<400> 375
acggatgcta cttgtccaat gatggtaaaa gggtagctta ctggttgctc tccgattcag 60
gttagaatga ggaggctctg ggctaggagt caataaagtg attggcttag tgggcgaaat 120
attatgcttt gttgtttgga tatatggagg atggggatta ttgctaggat gaggatggat 180
agtaataggg caaggacgc ccttagcttg ttagggacgg atcggagaat tgtgtaggcg 240
aataggaaat atcattcggg cttagatgtg ggaggggtgt ttaaggggtt ggctagggtg 300
taattgtctg ggtcgccctag gaggtctggt gagaatagt ttaatgtcat taaggagaga 360
atgaanagaa gtaagccgag ggcgtctttg attgtgtagt aagggtggaa ggtgatttta 420
tcggaatggg aagtgattnc taaggggntg tttgancccc gtttgtgcca gaatangaag 480
tggaatgctt cttanggctt caataaatga anggcanaat gaattgaaag gtaanaaac 540
cntnaagggg ggacttggtta ctgataaccn tccataaactc attgccccgn aacttggccg 600
gg                                     602

```

```

<210> 376

```

<211> 611
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> misc_feature
 <222> (1)...(611)
 <223> n = A,T,C or G

```

<400> 376
acgcgggcatc gaagaattca caaaaaacaa tagcctcatc atccccacca tcatagccac      60
catcacccctc cttaacctct acttctacct acgcctaata tactccacct caatcacact      120
actccccata tctaacaacg taaaaataaa atgacagttt gaacatacaa aaccaccccc      180
attcctcccc acactcatcg cccttaccac gctactccta cctatctccc cttttatact      240
aataatctta taaaaaaaaa aaaaaaaaaa aaaaaaaaaa ncaaaaaaaaaa aaaaanaaaa      300
aaaaaaaaang tncngccatt tttngttttn ggtaaacngg aatataangn gaaagaacaa      360
acnttggaac atacttaatg gattttttata gaactttgna aaccaaagga gattcatgtt      420
ttanaagtct ggcccttttt atatcttgga agaaaattat gtntggaggc tntaaataaa      480
tcccattatt ttctcaggga atctgggtag gaattgccgg catgggaant tttnnngggc      540
cggatnggaa agtttggcct aanaaatngc nctttntnaa naattttgga attttgggaa      600
gccnaagca n                                     .-          611
  
```

<210> 377
 <211> 367
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> misc_feature
 <222> (1)...(367)
 <223> n = A,T,C or G

```

<400> 377
acgcggggccg tttggcatct ctgccctcat cgtgggtttc gactttgatg tcactcctag      60
gctctatcag actgaccctt cgggcacata ccatgcctgg aaggccaatg ccataggccg      120
gggtgccaaag tcagtgcgtg agttcctgga gaagaactat actgacgaag ccattgaaac      180
agatgatctg accattaagc tggatgatcaa ggcactcctg gaagtgggtc agtcaggtgg      240
caaaaacatt gaacttgctg tcatgaggcg agatcaatcc ctcaagattt taaatcctga      300
agaaattgag aagtatgttg caaaaaaaaaa aananaaatn aaanaagtag ctcgcccgng      360
accacgc                                     .          367
  
```

<210> 378
 <211> 611
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(611)
 <223> n = A,T,C or G

```

<400> 378
ggtagctgga tcctgctcct ctgggttgaa acccgggcgc cgccaagatg ccggcttacc      60
  
```

actcttctct	catggatcct	gataccaaac	tcacggaaa	catggcactg	ttgcctatca	120
gaagtcaatt	caaaggacct	gccccagag	agacaaaaga	tacagatatt	gtggatgaag	180
ccatctatta	cttcaaggcc	aatgtcttct	tcaaaaacta	tgaaattaag	aatgaagctg	240
ataggacctt	gatatatata	actctctaca	tttctgaatg	tctgaagaaa	ctgcaaaagt	300
gcaattccaa	aagccaaggt	gagaaagaaa	tgtatacgct	gggaatcact	aattttccat	360
tcctggagag	cctgggtttc	cacttaacgc	aatttatgcc	aaacctgcaa	acaaacaggg	420
aagatgaagt	gatgagagcc	tatttacaac	agcttaaggg	caagaaactg	gactggaact	480
ttgtgaagaa	gttttcgacc	cttagaatgg	ttaaaccnac	agtgggggga	cttgcttttg	540
gaaaanaccg	tttattgacn	anagtttttt	tggactggan	atgaaaggng	ccnggttng	600
ccccggtttn	n					611

<210> 379

<211> 602

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(602)

<223> n = A,T,C or G

<400> 379

acagctgggt	ggacctattc	atgcatcttc	accagcagct	ggagcatctc	cacccttggg	60
atctctgggt	taaattactt	gagctctgtg	ctttgaaacc	agtttgataa	gtcctttact	120
aaggagctcc	tgaagggctg	ccctggccag	ggagcctcga	atcttcagtc	tctcagagac	180
cacagctggg	gttataagtt	tatagttggg	aacttcctta	cagagtttat	cataggtagc	240
tttgtcaaac	aagactaagt	tattgagctt	gtcccgaact	ttgcctttgg	accactttct	300
ctttttggcc	ttgcccccg	atgtgttcac	tgggtctttg	nctttcttgg	ccgactttcc	360
agcgtccttc	ttcttcttgt	cgtccttagg	cggcattgcc	aagctcggag	aatagcanca	420
gacacngnaa	cctngtcaag	atgtcngaca	aaaagccccg	ggtaccttgg	gcnngaacac	480
gcttaaggcg	aattccacac	actggcggcc	gtactanggg	gatccagctt	nggaccaact	540
tggnggaaac	atggcnaact	gnttcctngn	ggaaaatgtn	atccgttaaa	attnccccaa	600
at						602

<210> 380

<211> 598

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(598)

<223> n = A,T,C or G

<400> 380

ggtacngcgg	ggggtgcctg	gctccgtttc	ctgcttttgg	ttcttacagt	agtcggcgta	60
ggccttagat	tttttactgt	ctcctgaaga	atttaacaca	aacatggata	tcagacccaa	120
tcatacaatt	tatatcaaca	atatgaatga	caaaattaaa	aaggaagaat	tgaagagatc	180
cctatatgcc	ctgttttctc	agtttggtca	tgtgggtggac	attgtggctt	taaagaccat	240
gaagatgagg	gggcaggcct	ttgtcatatt	taaggaactg	ggctcatcca	caaatgcctt	300
gagacagcta	caaggatttc	catttttatgg	taaaccaatg	cgaatcagta	tgcaaaacag	360
attccggata	taatatcaaa	aatgcgtgga	acttttggtg	ccaagaaaag	aanaaagaaa	420
agaaaaagnc	caaacttggg	aacaactgna	caaccncaac	caaaaanctg	ggcnngggac	480

tccaaatcac ttatacccag ggaattcacc ccnaatctta ggtcctgata ctttcaacta 540
tatttaatcc ttaaaactta nccgaagagc taatngatga tgtntcctgc cggtaacn 598

<210> 381
<211> 631
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(631)
<223> n = A,T,C or G

<400> 381
ggtagcgagg gagagtgtgg tcaggcgagg cggactgagc aggactttcc ttatcccagt 60
tgattgtgca gaatacactg cctgtcgcct gtcttctatt caccatggct tcttctgata 120
tccagggtgaa agaactggag aagcgtgcct caggccaggc ttttgagctg attctcagcc 180
ctcgggtcaaaa agaattctgtt ccagaattcc ccttttcccc tccaaagaag aaggatcttt 240
ccctggagga aattcagaag aaattagaag ctgcagaaga aagacgcaag tcccatgaag 300
ctgaggtctt gaagcagctg gctgagaaac gagagcacga gaaagaagtg ctttagaagg 360
caatagaaga agaaccacaa cttcgtaaaa atggcngaag aagaaactga ccnccaaaat 420
gggagcttat taaagagaaan ccagangnnc caatngnttg gccaaactgg accgtttgca 480
anaagaagggt ttagcccnt tgaanaaatg ccggaagaac caaagaattc caagaccctt 540
gntgcnaaac ttgaacttgc ctaattgggtc ttgagaactg cttttttccc atcccttcta 600
aatccaaaa atgnacctgc ccgggggccc t 631

<210> 382
<211> 613
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(613)
<223> n = A,T,C or G

<400> 382
acattcccag atttttaagc ctccctcata aacacctgta atcagatcag agtgagaaga 60
aaagcttttt gaaactatgt tttctccagg gaagttctct tccaacaaga tggttttcac 120
tactgataac ttaacatgct ggaaacctgg taatgtttct atgactttat tttctaacc 180
cttctttaaa tctttaggca tagcatgctc tttggcagct ctcaaggagg gctgtttcca 240
tgtggctcca agttccttga actgctggct gcactgagtg gactgtctgt gtcttgagag 300
ggagctgcat tttcattgac ttatgggtccc acaagtgacc ctgaggcaan gtcnaattgg 360
tctncanaac atttttggcc ctctcttctc ctttttgact tttctgagac tgacagttc 420
tttganggaa tccaggggna angcttcctt ctctaattgg ggntaaattc attttccaaa 480
anggnccggt tttgggaaaa tnaaanttga aanggcattc nttttattaa tgccccnanc 540
ttttaanttc ngattntnaa cttnctgnta gaatttgtgg atccnccaaa ttggcttaat 600
attcaaatag ctt 613

<210> 383
<211> 628
<212> DNA
<213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(628)
 <223> n = A,T,C or G

<400> 383
 ggtactttga ccctggaaag gtatgggtct gcttaaaaga aagaagaaac atacacgtaa 60
 tcaaataaag cttaacatta tgcagggtct ataatacattt tcagcaacgg actgcaagct 120
 gcaactgtgaa gaaaatgcat agcagaggag aaagctgggg atctgaggaa ataggttaagg 180
 aaaacagtgt caacacacag tggaagaagt gatgaagaca tctattccgg agctcacgtg 240
 ccatgccctg ctagcgttcc ttaacaagcc acctgctcca gaaggccaca gcctgaccct 300
 cccaagtgga atataaatgc ccaagtgccca catgaagcca ccttctncac tacctaaaaa 360
 ggttgtctgg gactgagctc agaacacaca cctttctggg ctaccaaacc ttttaagtga 420
 aagaattttt tncataaatat ctanttttna taccactttt aacgccactt ttatattgaa 480
 attgggcttc taattagncc ctttcctcaa ttccttagga nggaactcat aatgggagcc 540
 aaccaaccag ggattctacc cccaatngac tgnnctttaa angattattt aattttgang 600
 ggcaaagggtg tgaatgggtt acaatacc 628

<210> 384
 <211> 620
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(620)
 <223> n = A,T,C or G

<400> 384
 acaggtaagc cctggctgcc tccaccact cccagggaga ccaaagcct tcatacatct 60
 caagttgggg gacaaaaaaa gggggaaggg ggggcacgaa ggctcatcat tcaaaataaa 120
 acaaaataaa aaagtattaa agcgaagatt aaaaaaattt tgcattacat aatttacacg 180
 aaagcaatgc tatcacctnc cctgtgtgga cttgggagag gactgggcca ttctccttag 240
 agagaagtgg gngggtttt angatggcaa gggacttctt gtaacaatgc atctcatatt 300
 ttggaatgac tattaaaaaa acaacaatgt gcaatcnaaa gtctcggccc atttgcgga 360
 ctttgggggg atgcttgctt cnaccgantt ggtgncaacc tttnnccggt tccanttttt 420
 naaattctta gttnaagcnn aaaaanntag aatancncna nancataact tannaancca 480
 tttaanaggt cctcggccg gaacnnnctt aanggtnaat cccantnnnt ggcgggctgt 540
 actnnggat ccanccttg nnccaaantn gnggaattca tggcnnaacc gntcctgggn 600
 gaantngttt ccttnaaanc 620

<210> 385
 <211> 535
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(535)
 <223> n = A,T,C or G

<400> 385

```

ggctacttttt tttttttttt tttttttggt atttagtttt tatttcataa tcataaactt      60
aactctgcaa tccagctagg catgggaggg aacaaqgaaa acatggaacc caaagggaac      120
tgcagcgaga gcacaaagat tctaggatac tgcagcaaaa tgggggtggag ggggtgctctc      180
ctgagctaca gaaggaatga tctgggtggt aagataaaac acaagtcaaa cttattcgag      240
ttgtccacag tcagcaatgg tgatcttctt gctgggtcttg ccattcctgg acccaaagcg      300
ctccatggcc tcacaatatt catgccttct ttcactttgc caaacaccac atgcttgcca      360
tccaaccact cagtcttggc agtgcagatg aaaaactggg aancntttgg ggtngggncn      420
acatttgctt tggccaaaat gccnggaacc ggcccgtac cttgncnng ccggccggtt      480
caaaagggcg aattccacac acttggcggg ccgtactang gggatccaac ttcgg      535

```

```

<210> 386
<211> 642
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(642)
<223> n = A,T,C or G

```

```

<400> 386
acagcattgg cagtgggtgcg tcagaggtgg cagaactatt tcacactaac cagttgaaga      60
ctacacaaga ttaataccat ccagcatcag gatatagctg tggattttac aaaccattct      120
tattttctaac ttcaggagtt gatgtttttc ccagtcctac ttaaaatatt actgctttaa      180
tcacagatca ggtaaaaagg acaacatgca caacctccac ctagaatcct gttgtagcct      240
agacagtga atgatatgac atcagaagac tttaaaattg cagctccttt tggatcccc      300
aaagtgtatc tgcactcttc ttcaaacggg cctcttttcc tcaagaagtc agaagtcacc      360
ttcacaangn ctgagaattc cattctgnnc ccaaantgca agggacactn aaggaagaca      420
tcattctttt attccgtnaa agacccttaa ttcattggng gaaactgggt gcacccgcct      480
nagaatcttt attanactct ttgnccaatt tggttacaga agagntncan tanccccang      540
aannggtagc ctttgaggtt tgantcacc tcataagcac ccttaaacca cctgnttggg      600
gaaccttctt tcaactgtcc ctaactttat tangccctaa ag      642

```

```

<210> 387
<211> 256
<212> DNA
<213> Homo sapiens

```

```

<400> 387
ggaccttttt tttttttttt tttttttttt tgaaaagaaa ggccttacat atttattact      60
gaatccagcc aaccaacgtg ttcataacag attcagagag gaaaacacgt cgaaatctcc      120
agatagtggg gacattttca gcttgatatg gtaacatgat cgtgaccttc agacagcata      180
aatatgtgtg ccatctcatg tgcaattcct tatagaccca gcttggttct tctccaatgt      240
ctccttttgg agttgt      256

```

```

<210> 388
<211> 566
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(566)

```

<223> n = A,T,C or G

<400> 388
 ncnagcggcc gccngncng gnactgaaca ttggtaaaaa attatatgag ggtaaaacaa 60
 aagaagtcta cgaattgtta gacagtccag gaaaagtcct cctgcagncc aaggaccaga 120
 ttacagcagg aaatgcagct agaaaaaac cacctggaag gaaaagctgc natctcaaat 180
 aaaatcacca gttgtathtt tcagttatta caggaagcan gtattaaaac tgccttcacc 240
 agaaaatgtg gggagacagc tttcattgca ccgcagtgtg aaatgattcc aattgaatgg 300
 gtttgcacaa gaatagcnac tggttctttt ctnaaaagaa atcctggngt caaggaagga 360
 tataagtntt accccctaaa gtggagntgt ttttcaagga tgatgcccat taatgaccnc 420
 cagtcgggct tgaagaacna cttgattgct gcaaaaattt gcttttcttg gacttcttat 480
 anggcnaacc tgaa. ggat ttcatgaagt catgctacnc aggcctatatt tgaaatctgg 540
 gagaaatcct gggtgcccac aattgg 566

<210> 389

<211> 629

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(629)

<223> n = A,T,C or G

<400> 389
 actttttttt tttttttttt ttttttgttt tttttttttt tttttttttt ttttttttgc 60
 agttttctaag tcattacttt tnatttttgaa agatttgnga aactnttcac atcatggtga 120
 gagtttgtat gattaataan aagcagcttt ttcattgaaat gcttggaggt gaacgagttn 180
 tcagcctgng anatecgacc ntcccattaa ctttgaagtt tctcttgatt aatagaagaa 240
 aaaaggggag ggtgaanaaaa aggaggaaca tgctaaaaac cttatgacaa tcatccaaat 300
 gtgaggaaag aacaacccga ttcaccaact ccactttttt tattttacaa ctttctacat 360
 ctcacncttg gattttggcc ttcntggctn aaacantcct ggcantccnt tanagccctt 420
 gaaaaagagc cntggntttt ncaaaagacn ntnggnnggn gaannccctn annatgcctt 480
 gaccntttn cnaagaactn nntntccggg ntcccaaaag tttgacccan cagcttantg 540
 tgaannnaaa actnnccttn aaaggtaatg ggnggaanng gtgannaant ggggtttttt 600
 ganaagtctt ntttttctna aaacnccg 629

<210> 390

<211> 596

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(596)

<223> n = A,T,C or G

<400> 390
 actttaattt attttccctt tctagtgtat taagaaatga catgcacttt aatttgccaa 60
 aagcaatgct tgtattctgg cagcaacatg ctacttctat cacatagtaa agtgaatacc 120
 agaactacaa aggcaggagg tgtaagtga tttttattgg gaggggaggt tggcaactta 180
 aacagcagca aataaagagt gaataaggaa actcctgtt gccacagata cacaagacct 240
 ccgtatgtga tacaggagcc atttcaattt gtgaccctta gacagagatg gcaagtgtct 300

ttccattcaa	tctaatactt	ccggattcct	actaaaaagg	aatcattaag	agcatggaaa	360
agttgcttac	tggaaaggaa	acccccgaag	agtaagggaa	gggaatgtga	aattaagaag	420
ttatgtggaa	tctcttaaat	tgnaattact	acattttctta	atttccaggt	atnccaaaca	480
cagtcctntg	caaaactggg	cagntactta	aatnccngat	ccatttttagg	cnttacataa	540
gtgtttggga	gtacctatgg	tatttnaatg	aactttttaa	ctttnttccg	ccgtcc	596

<210> 391
 <211> 625
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(625)
 <223> n = A,T,C or G

<400> 391						
acacacccag	gaaatttgtc	atccaccctg	agagtaacaa	ccttattatc	attgaaacgg	60
accacaatgc	ctacactgag	gccacgaaag	ctcagagaaa	gcagcagatg	gcagaggaaa	120
tggtggaagc	agcaggggag	gatgagcggg	agctggccgc	agagatggca	gcagcattcc	180
tcaatgaaaa	cctccctgaa	tccatctttg	gagctcccaa	ggctggcaat	gggcagtggg	240
cctctgtgat	ccgagtgatg	aatcccatcc	aagggaacac	actggacctt	gtccagctgg	300
aacanaatga	ggcagnttta	gtgtggctgt	gtgcaagggt	tccacactgg	tgaagactgg	360
tntgtgctgg	tgggtgtngn	canaggacct	ngntnctaaa	accnccgnnt	tgggcaatgg	420
ggctttcgtc	taattnttac	aannttgntg	accaatnggg	gatnaactgg	anntttttgn	480
tcaanactnt	tttggaataa	tntccctnnt	gcnattngcc	ntatttcctg	gggaanggtg	540
ttnatatngt	natggnnaaa	cntntanccg	nnntntaatc	ttggaatata	tatnaatacc	600
ttcttaaaan	ntgntnatta	tcctt				625

<210> 392
 <211> 266
 <212> DNA
 <213> Homo sapiens

<400> 392						
ggtacccata	ttgctaattgc	taggatcaag	ataccacata	gccagaacaa	gaagttgaag	60
gtaaacatag	aatattttat	acaggcactc	acacctgcca	tttcggaaaa	ggattaggaa	120
tccagatgcc	gtgaatttaa	ctattcgtaa	caggcttgct	ctgcaatatg	ctctggagca	180
acttgctgc	agagattttc	gtatccacgg	cttcagagca	gaaagagaaa	gcaaagaagt	240
agagggagga	ataaaaaatcc	ccgcgt				266

<210> 393
 <211> 611
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(611)
 <223> n = A,T,C or G

<400> 393						
ggtacttttt	tttttttttt	tttttttttt	tggtttttacc	tggtttttatt	ccttaaaaaga	60

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aaaaaacaac ttaaatgcat acatacagaa tagaatacac ttacttaagt tttgacagtg 120
aaaaaaaaata attacagggt agatattttaa tccaagggtt aacatgggga tgatctcata 180
aggcaatttc tttccttttaa taaatatttaa agtgaatatt attctggaag caaatcatct 240
cctaattctt catcagcaaa atcatcctca tcgacccctt tcttggtctg agtttttggt 300
cgttctatct gagggccaag tgggtccaca taggaggcat ctatttcttt gntactgcta 360
ctttcataag gntcatttgt cccaggtaaa agctctgagt ctggccttan tccgtcacc 420
tttactactg gcncatatag ctggccacta tnaacgntag ccttncctnt cnttttgna 480
cngggagcccc caatgcannt ttngontgac tttagcncng gncctaatt cttcattttt 540
ccacctttna gnttttgga antcttgagc cntttttaat cnaagacttn gcanagccaa 600
ttaaaaaccc c 611

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<210> 394

<211> 340

<212> DNA

<213> Homo sapiens

<400> 394

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acgagtccca ctatgcgctg cccctggguc gcaagaaggg agccaagctg actcctgagg 60
aagaagagat tttaaacaaa aaacgatcta aaaaaattca gaagaaatat gatgaaagga 120
aaaagaatgc caaaatcagc agtctcctgg aggagcagtt ccagcagggc aagcttcttg 180
cgtgcacatgc ttcaaggccg ggacagtgtg gccgagcaga tggctatgtg ctagagggca 240
aagagttgga gttctatctt aggaaaatca aggcccgcaa aggcaaataa atccttggtt 300
tgtcttcacg caaaaaaaaa aaaaaaaaaa aaaaagttacc 340

```

<210> 395

<211> 557

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1) ... (557)

<223> n = A,T,C or G

<400> 395

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acacatcttc aaagcacttc cctttaacgg gaaacttagc tttatgggat ttaaacatta 60
gaaagtggga aaaaaaattc cttttcttg tcattataaa ccaaaacaaa atctagtgt 120
agtcaaggaa actcattcac acttcaggtc cttctcctcc aggaaccagc attgttatat 180
tatttccatt tagcaaaatc tgatgtaatt tagtaatcct tcttccttct ggtgtgattt 240
caaactcagt gacatcttcc agtactttnt tttttttttt ttttttttgg gtgttgagct 300
tggacgcttt cttaattggg ggtgcttttt aggcctacta tgggtgttaa atttttactc 360
tctctacaag gntttttcct agtggccaaa agaagctggt ccctcttttg gactaccggt 420
aaaattacca nggggattta aaangggnt tnggggcaa attnaagtt ngactangan 480
tctatttttg gcccaaccagt nttaaccagg cttcggtang gttggccgcc cccgggtacc 540
ttgggccggg aacacnc 557

```

<210> 396

<211> 617

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(617)

<223> n = A,T,C or G

<400> 396

ggtacngcgg	ggccactcga	gtgcgcaggc	gcctggcgat	taccgggtctc	accatggagc	60
ggaaagtgct	tgcgctccag	gcccgaaga	aaaggaccaa	ggccaagaag	gacaaagccc	120
aaaggaaatc	tgaaactcag	caccgaggct	ctgctcccca	ctctgagagt	gatctaccag	180
agcaggaaga	ggagattctg	ggatctgatg	atgatgagca	agaagatcct	aatgattatt	240
gtaaaggagg	ttatcatctt	gtgaaaattg	gagatctatt	caatggggaga	taccatgtga	300
tccgaaagtt	aggctgggga	cacttttcaa	cagtatgggt	atcatgggat	attcagggga	360
agaaatttgc	ggcaatgaaa	gtagttaaaa	gtgctgaaca	ttacacttga	aaccagccta	420
gatgaaatcc	ggttgcttga	agtcagttcc	aattcagacc	ttatggatcc	aaatngaaaa	480
atggttgtca	actactagat	gactttaaaa	ttcaggaggt	aatggaacac	atatttgcac	540
gggatttgaa	gttttggggc	anattngtta	agnggttctc	aatcaatttn	ttangggcct	600
tcctgccttg	ggtnaaa					617

<210> 397

<211> 594

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(594)

<223> n = A,T,C or G

<400> 397

acgcggggga	tcaggactcc	tcagttcacc	ttctcacaat	gaggctccct	gtcagctcc	60
tggggctgct	aatgctctgg	gtcccagggt	ccagtgggga	ccgtcgtggt	gactcagtct	120
ccggtctccc	tgcccgctac	ccttggaacag	ccggcctcca	tctcctgcag	gtctggtgaa	180
actctccttt	acgaagatgg	aagcacctac	ttgagttggt	ttcaccagag	gccaggccaa	240
tctccgaggc	gcctgattta	ttaaagtttct	aaccgggact	ctgggggtccc	agacagattc	300
agcggcagtg	ggtcaggcac	ttattttcacg	ctgaaaatca	acagggtaga	ggctgatgat	360
gttggggaatt	attactgcat	gccanggtca	aactggcccc	tcacttttctg	gngaaggacn	420
aaaggtggcc	natcaaacca	actgnggctt	gaccattggc	ttcatnttcc	cgccatttga	480
taaccantga	aatctggact	gctttgtggg	ngcctgctga	aaacttntat	nccnanaggc	540
cnaagtcag	acagtttttc	nattttactcg	aaaaatntgg	aaatgataat	tttn	594

<210> 398

<211> 611

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(611)

<223> n = A,T,C or G

<400> 398

acagtggctcc	ttttcagagt	tggacttcta	gactcacctg	ttctcactcc	ctgttttaac	60
tcaaccagc	catgcaatgc	caaataatag	aattgctccc	taccagctga	acagggagga	120
gtctgtgcag	tttctgacac	ttgttggtga	acatggctaa	atacaatggg	tatcgctgag	180
actaagttgt	agaaattaac	aaatgtgctg	cttgggttaa	atggctacac	tcactctgact	240

```

cattctttat tctatttttag ttggtttgta tcttgccctaa ggtgcgtagt ccaactcttg 300
gtattaccct cctaatagtc atactagtag tcatactccc tggtagtagt tattctctaa 360
aagctttaaa tgtctgcatg cagccagcat tcaatagtga atggncctc tttggctgga 420
attaccaaac tcagagaaat gnggcacatg gagaacatct taaccccatg aanggataaa 480
agccccaat ggnggggact tgataatagc nctaattgctt taaanatttg gtccactttt 540
tacctaaggt gagccattg aaccannggt gctaaangct catacttcca actgaaatgg 600
ttaaggaaaa a 611

```

<210> 399

<211> 614

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(614)

<223> n = A,T,C or G

<400> 399

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actctgtgaa tggtagagag ctgggcacct acatgggccca taccggagct gtgtggtgtg 60
tggacgctga ctgggacacc aagcatgtcc tcactggctc agctgacaac agctgtcgtc 120
tctgggactg tgaaacagga aagcagctgg cccttctcaa gaccaattcg gctgtccgga 180
cctgcggttt tgactttggg ggcaacatca tcatgttctc cacggacaag canatgggct 240
accagtgtt tgtgagcttt tttgacctgc gggatccgag ccagattgac aacaatgagc 300
cctacatgaa gatcccttgc aatgactcta aaatcaccag tgctgtttgg ggaccctng 360
gggagtgcat catnctggcc atgaaaagtg gagagctnaa ccagtattag tgccnagtt 420
tnnanaaggt gttngttnaa tgttaaagga gcantttccg gnagaataac cnacnttcag 480
gttattccnn gganatgacc anngtttnga ccccttnnaa gtccattaat nccnaacttt 540
tttacnctca aatttttnaan tnanaaaact tttngnatna aattnttnaa ttanttgttc 600
tttttcaata tnnn 614

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<210> 400

<211> 612

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(612)

<223> n = A,T,C or G

<400> 400

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acttacactg tgaaatttta tgatggagta gtccagactg tcaaacatat tcatgtcaaa 60
gctttttcca aagatcaggc cttaaagaaac agatcacaaa agtctttcat catctcctga 120
taaacgagag aagtttaaag aacagagaaa agcaacagtg aatgtgaaga aagacaaaga 180
agataaaccc ttaaagacag aaaagcgacc caagcagcct gataaagaag gaaagttaat 240
ctgttctgaa aaggggaaaag tgtcagagaa aagtcttccc aagaacgaga aggaagacaa 300
ggaaaacatt tccgaaaatg acagagagta ttctggagat gcccaagtgg ataagaaacc 360
tgaaaatgac attgtgaaga gtccacaaga aaacttgagg ggaaccnaaa ngaaaacgag 420
gcagaccccc ttccatagct nctactgctg gggattnaaa ctttaaactt tggcacccat 480
acctttggac ttnnnanaag gaaaatttca naggggtgtga agtcctttta accgtccttg 540
gttgncaaaa ntttttncng ggaaagtcaa aaacttcttt gaaaaccttg ccnangattt 600
ttnngngnac nt 612

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<210> 401
 <211> 601
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(601)
 <223> n = A,T,C or G

```

<400> 401
ggtacggtaa ctgactccag ggtcactcat actgtgtccg tggtaacggt aagtctgcag      60
ctccatcagg atgggccccct tcccagatct acaataggca gcagcaaacc ttgttgccctc    120
tcggacgcac aggatatcca ttccatccac tctcagacca ggaatgaaat cgcctctctt    180
gtagtaatca gtgctggctg ccgctctctc aacagacggt cccattccat agcgattatt    240
ctcacagatg aaaatacaag gtaatttcca caaagctgcc atgttgtaag cttcgaatat    300
ctggccctgg ttagcagcac catcgccata taaagtcagg cagacctcat cttttccatt    360
atacttacag gctagagcaa tcccagcgcc caagggcacc tgcgctccta cgatgccatg    420
gccccgtana agtcttggca tacatgtgca tcgactctcc ttcccttagc acaanctcct    480
tttgnccgtg aactgcaaaa tttntcggac ggaaaggccc cggtgnaaag taaagccgtg    540
agccccgnag gctgngatna aanggcctgt ggggttnaag cccggcttca ggtcccacag    600
a
  
```

<210> 402
 <211> 600
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(600)
 <223> n = A,T,C or G

```

<400> 402
acctggagaa gatcaaacag cgactgtttg agaaccttag aatgctgccg cacgcacctg      60
gggtccaaat gcaggcgatt cctgaggacg ccacccctga ggagagtggc cgatgaggac    120
gaagacgacc ctgacaagcg catctcgatc tgctcctctg acaaacgaat tgctgtgag    180
gaagagttct ccgattctga agaggagggg gagggggggc gcaagaactc ttccaacttc    240
aaaaaagcca agagagtcaa aacagaggat gaaaaagaga aagaccaga ggagaagaaa    300
gaagtcaccg aagaggagaa aaccaaggag gagaagccag aagccaaagg ggtcaaggag    360
gaggtcaagt tggcctgaat ggacctnttc agctctggct ttctgctgag tccctacgtt    420
ctttcccaac cccttaaatt tataatttct attctctggg gatttatata aaaatttatt    480
naatnttaat attcccagg cccgaaacca agggcccgaa ctnaaggnaa ntttgcttgg    540
gtgagctntt tcaagaacca ccttgacacc atttttccgt cttaacttta accaaaangg    600
  
```

<210> 403
 <211> 604
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature

<222> (1)...(604)

<223> n = A,T,C or G

<400> 403

actcagtgga	tgacgagtg	ttggtgaaat	tggtgaaaagg	cctgtgtctg	aaatacctgg	60
gccgtgtcca	ggaggccgag	gagaatttta	ggagcatctc	tgccaatgaa	aagaagatta	120
aatatgacca	ctacttgatc	ccaaacgccc	tgctggagct	ggccctgctg	cttatggagc	180
aagacagaaa	cgaagaggcc	atcaaacttt	tggaatctgc	caagcaaaac	tacaagaatt	240
actccatgga	gtcaaggaca	cactttcgaa	tccaggcagc	cacactccaa	gccaagtctt	300
ccctagagaa	cagcagcaga	tccatggtct	catcagtgtc	cttgtagctt	tgtgcagcag	360
ttccgggctg	gaagacagag	acagctggac	agagctcctg	aaaacatttc	aaaaataccc	420
ccttcccctg	gcctgccctg	cctttggggt	ccancggcac	ttcagttgga	tggcacaacc	480
tantgtatcc	gtgcnnaaan	cnaacctggc	attttcaccc	anntanccaa	gggcttttgc	540
caagggnana	acagtggagc	ccttggcttg	ncctataaac	atacgggtac	cttggccgnn	600
acnn						604

<210> 404

<211> 604

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(604)

<223> n = A,T,C or G

<400> 404

ggtactttgt	ggataagaaa	atggaggaac	acatctgatg	gagagtgggc	atttgacaac	60
aatggaacag	gtaaccagca	tgtaaaatca	aaatataagt	gtctttttta	gagctgaaag	120
ctgctgctgg	tcattcatta	atgtgtcaga	catttaatca	ggatgctgga	ccttcaaaat	180
aactgaaaaa	agaaccaaga	aaaggcggtt	ttgttttcaa	caaactttac	taaaataccc	240
cggaaaggca	atgaacgatc	tgacaattta	agctctaattg	atttaaagct	cagctagaag	300
aaagtgaggc	atgacatata	ctgtcaacgg	aggggtgaagg	aggcagattt	ctggaaatgc	360
aatgatccca	cacatttgct	tcaaggagaa	acctgcagac	atattttcag	gtcttgctaa	420
gtaacaactg	gttatttgta	atcaatcatt	tgggaaagtc	tgctatgtag	ctaanggcac	480
tgtgaccccn	gacaacngat	gaaaaggaaa	aagcmttgac	agcaggaaaa	atccttccat	540
cttaaagaat	ttagggggaca	ccttttaaagg	aaaaaaattg	ntccagcctc	atttttacaa	600
ntnt						604

<210> 405

<211> 593

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(593)

<223> n = A,T,C or G

<400> 405

acttgcattt	caaagcttat	aagatataaa	tggagatttt	aaagtagaaa	taaatatgta	60
ttccatgttt	ttaaaagatt	actttctact	ttgtgtttca	cagacattga	atatattaaa	120
ttattccata	ttttcttttc	agtgaaaaat	tttttaaattg	gaagactgtt	ctaaaaatcac	180

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ttttttccct aatccaattt ttagagtggc tagtagtttc ttcatttgaa attgtaagca 240
tccggtcagt aagaatgccc atccagtttt ctatatattca tagtcaaagc cttgaaagca 300
tctacaaatc tcttttttta ggttttgncc atagcatcag ttgatcctta ctaagttttc 360
atggggagac ttccttcac acatcttatg ttgaaatcac tttctgtagt caaagggtata 420
ccaaaaccaa tttatcttga actaaattct aaagtatggg tatccaacca tatacatctg 480
ggtaccaaac ataaatgctg acattcntat attatagtna aggcttaatc naattgcagg 540
tgaatggaaa aaaaataagc ttnaacctag gattctggaa tgaggaatgc tcn 593

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<210> 406
 <211> 591
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(591)
 <223> n = A,T,C or G

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<400> 406
actttttttt tttttttttt tttttttttg ggactgaatc ttgctctgtc gccagggctg 60
gagtgcagtg gcgcaatctt ggctcactgc aacctctgcc tcctgggttc aagtggttct 120
catgcctcag cctcctgggt agctgggatt acagacaagc accaccacaa ccagctagtt 180
ttttttgttt tgtttttttg agacggagtc tcgctctgtc accagggctgg agtgcagtgg 240
cacaatcttg gctcactgca acctctgcct cctgggttca agagattctc ctgcttcagc 300
ctnccaagta gctgggacta caggtgcaca ccatcacacc tggctaattt ttgtattttt 360
aagtanagac ggggtttcac catgttggcc aggcctggct caaactcctg acctcaagtg 420
aaccggccgc ttancttcca aagtgcctggg attacaggcg tgagccact ggctggctg 480
accatttggt tattaacagg gcccacaana tgcnccttta ngtgaaaggg natggcccca 540
gggaacaatt nngctgaaaa acaccaaagg ccnantccat aattcnttgg n 591

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<210> 407
 <211> 463
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(463)
 <223> n = A,T,C or G

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<400> 407
ggtactgatt ttaaaaaacta ataacttaaa actgccacac gcaaaaaaga aaaccaaagt 60
ggccacaaa acattctcct ttccttctga aggttctacg atgcattgtt atcattaacc 120
agtcttttac tactaaactt aaatggccaa ttgaaacaaa cagttctgag accgttcttc 180
caccactgat taagagtggg gtggcaggta ttagggataa tattcattta gccttctgag 240
ctttctgggc agacttgggt accttgccag ctccagcagc cttcttgctc actgctttga 300
tgacaccac cgcaactgtc tgtctcatat cacgaacagc aaagcgaccc aaaggtggat 360
agtctgagaa gctctcaaca cacatgggct tgccaggaac catatcaaca atggcagcat 420
caccagactt caagaattta nggcatctt tcccgggtac ctg 463

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<210> 408
 <211> 588
 <212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(588)

<223> n = A,T,C or G

<400> 408

acaaatatat	ataaattaca	tttgattgta	aggccaacgt	tcaaaagtaa	aaatgagatg	60
agctctctta	ttgttatccg	aggtaacagag	gctgcaactg	tcaaggggat	gttctcacca	120
aaaggggggt	tgggggaaga	ggacacacac	aaagctaata	aaaccagaat	ccccatcccc	180
acaaaactca	tgggaacaaa	atttaaagga	taaaacaaaa	cccaccaaga	cccatattac	240
aaaccaatat	ggtaacctgt	gttcccttct	atggtatgat	tatgtcatgt	taccttagtg	300
ttaaaagatt	aacataagga	aactgcagca	atatataaaa	gatataattct	ctatagagca	360
tatttcgatt	gattccatta	aaataatgac	attagaattc	catcatangg	ttaaaaccag	420
gacaataactg	nttttntttt	atttaaaaaa	aactaccacc	taatgactgn	attggtcata	480
acctgaatgg	tgtgcaatgg	gctcttccat	gaatggctgg	cngaacaag	cttgggncct	540
gcttgagttt	cagctttcct	ctttaattta	gtngctcaat	gataaaca		588

<210> 409

<211> 612

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(612)

<223> n = A,T,C or G

<400> 409

ggtacaaaga	tctgacatgt	caccagggga	ccattttcac	ccactgctct	gtttggccgc	60
cagtcctttg	tctctctctt	cagcaatggt	gaggcgata	ccctttcctc	ggggaagaga	120
aatccatggt	ttgttgccct	tgccaataac	aaaaatgttg	gaaagtcgag	tggcaaagct	180
gttgccattg	gcattcttca	cgtgaaccac	gtcaaaagat	ccagggtgcc	tctctctgtt	240
ggtgatcaca	ccaatttttc	taggttagca	cctncagtca	ccatacacag	ggtaccagtg	300
tcnaacttga	tgaaaatcaa	gtaatcntgg	ccagtctcta	aaatcaaata	ttgaatggta	360
tcaattcacc	cttgatgaag	gggaatcggg	ggtaaccggg	atgggtgccg	ggccttnatg	420
aagtcannca	natgaaggga	ttcctttggg	gcccccaaa	aacttttttn	attttcacaa	480
cttgnacctt	gccccggcgg	ccgttcacaaa	gggcnaattc	cagncacttg	gnggccgtct	540
aanggatcca	actcggacca	acttggcgna	anatggcaaa	ctgggttcctg	gggaaatggt	600
atccctccaa	tn					612

<210> 410

<211> 353

<212> DNA

<213> Homo sapiens

<400> 410

acgcggaagc	agtggttaaca	acgcagagta	acgcgggatg	gcacatgcag	cacaagtagg	60
tctacaagac	gctacttccc	ctatcataga	agagcttatc	acctttcatg	atcacgcctt	120
cataatcatt	ttccttatct	gttctctagt	cctgtatgcc	cttttcctaa	cactcacac	180
aaaactaact	aatactaaca	tctcagacgc	tcaggaaata	gaaaccgtct	gaactatcct	240
gcccgccatc	atcctagtc	tcctcgcctt	cccatcccta	cgcctccttt	acataacaga	300

cgagggtcaac gatccctccc ttaccatcaa atcaattggc caccaatggt acc 353

<210> 411
 <211> 612
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(612)
 <223> n = A,T,C or G

<400> 411
 ggtacgcggg gagagaaacc tggctttact atggcgggtg gaggaacggc agtgatcaca 60
 cgtcggctgc tgggaagatc tggattctcg tttcagggtc ccatcagaaa agctaagttt 120
 gctgtatagt gaggatcagg agatctgac ctgattgcag aaccttcctt gattacagaa 180
 tcttgggttg tatctccac ttcacccttc tagaccatcc cagaagatct ataagatttc 240
 atctgggaaa tcaactaggag ttcttgggaag ggaaagaagg aagattgttg gttggaataa 300
 aaacagggtt gaatgagttc cagaaagcnn ggttctcaac ctctgggaca gcaatctgca 360
 gaagangaga acttcaaaaa accnactana agcancttgc anagaagtaa aatgagaagg 420
 ggncttctna ngaaagaaga cacttggnc acagcagaaa aaactttgac cnantnttnc 480
 caggaagana ggggggggtc cnccttttaa naacccctt taagatncng gnggaanacc 540
 tcanngacca nccntaaatt nnggaaaccg aaaaggggcn gtcctttttg ntinncagntg 600
 cncnttaan nt 612

<210> 412
 <211> 607
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(607)
 <223> n = A,T,C or G

<400> 412
 acgcgggggt ctctcgccag gcgtcctcgt ggaagtgcga tcgtctttta accctgcgtg 60
 gcaatccctg acgcacggcc gtgatgccc ggggaagacag ggcgacctg aagtccaact 120
 acttccttaa gatcatccaa ctattggatg attatccgaa atgtttcatt gtgggagcag 180
 acaatgtggg ctccaagcag atgcagcaga tccgcatgtc ccttcgcggg aaggctgtgg 240
 tgctgatggg caagaacacc atgatgcgca aggccatccg agggcacctg gaaaacaacc 300
 cagctctgga gaaactgctg cctcatatcc gggggaatgt gggctttgtg ttcaccaagg 360
 aggacctcac tgagatcagg jacatgttgc tggccaatna ggtgcccagc tgctgcccg 420
 gctggtgccc atttgcccat gtgaangtca cttgtgccc gcccaaaaca cttgtcttng 480
 ggcccganaa gaacttcttt tttccaggcn ttaaaatatt caccctttaa antttcaagg 540
 ggccccattt gaaatcctgg annatnngca ttgatcaana ttganacaaa gtggnancnt 600
 ccaaccc 607

<210> 413
 <211> 606
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(606)
 <223> n = A,T,C or G

<400> 413
 acagggtcaga gtcttctttt cttttctttt tgagatggag tcttgctctg ttgccagact 60
 ggagtgcagt ggtgcgactt gggctcactg caatctccac ctcccgggtt caagcgattc 120
 tcttgccctca gcctcccagag taactgggac tacagggtgtg cgccaccaag cccagctcat 180
 ttttgatatt ttagtagaga tggggtttca cgatgttggc taggatggtc tcgatctctg 240
 gtcagagtct tttctgtaaa tatccttggg aaagaagaa ttttagactg tagctgttgc 300
 aaatgcttta aggaagaagc anaacaactg tcagtcttcc tgaaatgaag aaactacacc 360
 agggctgcta tatcagagca accccaacca gcactccaat catgatgccc gacagtggcc 420
 ccagcttgag aaccagagaa gttccagatg cagagactgt gagctcntga ctatgggaat 480
 tttngnggcn ntaacccaan tttgagacna aacnagcct tngnccggg tttnatttgg 540
 gngggatttt gcggataaan aaacttgngg gggntnctgc ggnatccatg gaacnccaaa 600
 anatng 606

<210> 414
 <211> 624
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(624)
 <223> n = A,T,C or G

<400> 414
 ggtacttttt tttttttttt tttttttttg tagatgagggt ctcgctatgt tgcccagggt 60
 ggagtgcagt tattcacagg tgcaaccaca gggcactgca gctttaaact cctgggctca 120
 agcgatcctc ctgcctcagc ctcccaaata gttgggacta gatgcacgca cnaccacgcc 180
 tgactcagga cattattctt aaagggtatta tccaggaaac agataagggtc attcataaaa 240
 cacacggntt ttttcttttag ctcatgtgta acaatgaaag tagattccac tattgaagca 300
 caagttgcaa attggtaaca tagngaacat attgntgtag gaaagggggg tcatgtgtnt 360
 gtgttatatn agcncttgaa ctttttatgg gngtnataag ccnngttatc ttgncccaaa 420
 gaaannccat ttttaggatt ngatggtttt cttannggaa nannctnggg ggnattntgt 480
 ngggcatgaa cttttatgtn ggaatcagtc ccatanaggt aaggggtttn aatcccaaaa 540
 ancggggnct tttatgggaa atnnccttta cttcaaaggc caaanngatn gtnggtgtca 600
 cttcnaantt ccngannnca anng 624

<210> 415
 <211> 609
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(609)
 <223> n = A,T,C or G

<400> 415
 acgcgggtta caacggaagt aaaatctgtc gaaatgcacc atgaagcttt gagtgaagct 60

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cttcctgggg acaatgtggg cttcaatgtc aagaatgtgt ctgtcaagga tgttcgtcgt 120
ggcaacngtt gctggtgaca gcaaaaatga cccaccaatg gaagcagctg gcttcactgc 180
tcaggtgatt atcctgaacc atccaggcca aataagcgcc ggctatgccc ctgtattgga 240
ttgccacacg gctcacattg catgcaagtt tgctgagctg aaggaaaaga ttgatcgccg 300
ntctggtaaa aagctggaag aaggccctaa attcttgaag tctggtgatg ctgccattgt 360
tgatatgggt cctggcaagc ccatgtgttg ttgagagctt tctcagacta tccacctttg 420
ggtngctttg ctggctcgtga natgagacag acaggtgccn gtgggggtggc atcaanncat 480
gggacaanaa aggccttnttg gancctgcaa aggtncncaa nttttgncca naagcntcaa 540
aagntaattg aatttttccc ctannnctg cnccttctt tannanggnn ggaaaacggc 600
ttaaanntt 609

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<210> 416
<211> 577
<212> DNA
<213> Homo sapiens

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<220>
<221> misc_feature
<222> (1)...(577)
<223> n = A,T,C or G

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<400> 416
ggtacgagct gattgggaac gggctccaat ggacatggct ctgcagtcaa aatagttagc 60
agatggacag gtttggaaaa tgtgagggcc catatcatca tanccagcaa taaggagacc 120
aacaccatat ggtctccggc catatccgtt gtgttggtat ctgggtcttg cttccaatta 180
gagatacaag actgagacac aggcagtggg ctatcgaata caaatctgga atncaaacac 240
tcctgacgca taaaattaca taacagncta gcatnancag taagcccccg caattgagat 300
accaatatgg ttgtcaacat ggagaatttt tttctgatga cctgccaaact cttgatttgc 360
gcccttttca atgcnaaccc aaaactggca tgaagntttt gnatttcaga ccancctgnt 420
ggctgnacct tggcttaaca ggtttccatt ggcntatttc natttggatn aantcttgcc 480
cntggggggn ttcnaancta ggggccatca nttggtcaaa ctgntttnta aaccatgggg 540
gcnngctcng gccttggttg ctggcntcaa caaaaaan 577

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<210> 417
<211> 570
<212> DNA
<213> Homo sapiens

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<220>
<221> misc_feature
<222> (1)...(570)
<223> n = A,T,C or G

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<400> 417
ggtactaaga atattagaga actggaaatc cagttttttt gtgggtttttt aagaaagaga 60
atctgactcc attgcccagc ttggagagca gtggtgcaat agctgggggt acaggcgtga 120
gccaccacac caggcctgga aaccagttt taatttgtga actacaaatg gttggcaact 180
gattccttaa ttgttattgc aggagttagc ccaacatgag tccatatgta gtccttctct 240
ggtctggttg gaactgtggg aaatgggtgat gaccgtgact tgaaataactn agaaggtgca 300
tgacaaacaa attccaagta ttccatcttc cttggaagat cttcctctgg ccctatgata 360
taggaagcng gaatcaaatt tgggctcttg ggctaagant aggggtatgg aatgagcccc 420
cgtnaantgg cttgnacttc ttcttcgcta atactgggcc ctggattaaa accttttgat 480
tnnancnata gntagggctt tccttcttgg ttaatcaatt cccagaaacc aacattccca 540

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atttgggtaa natactccct tgtanaaaaa

570

<210> 418
 <211> 570
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (1)...(570)
 <223> n = A,T,C or G

<400> 418
 ggtacttcta cacatctgcc taacttggga atgaatgtgg gagaaaatcg ctgctgctga 60
 gatggactcc agaagaagaa actgtttctc caggcgactt tgaaccatt ttttggcagt 120
 gttcatatta ttaaactagt caaaaatgct aaaataattt gggagaaaat attttttaag 180
 tagtgttata gtttcatgtt tatcttttat tatgttttgt gaagttgtgt cttttcacta 240
 attacctata ctatgccaat atttccttat atctatccat aacatttata ctacatttgt 300
 aagagaatat gcacgtgaaa cttaacactt tataaggtaa aaatgagggt tccaagattt 360
 aataatctga tncagttctt gntatttccc aatagaatgg gactnngnnc tgtaanggc 420
 ttaagganaa agggaagata agggttaaaa gttggttaat ggaccaacc nttnaaaga 480
 aatgcnntan anaatanntt natgantaaa naaaggtncc tngccnnggc cggccggttt 540
 aaangggcca atttcnagca cncnnggcg 570

<210> 419
 <211> 574
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (1)...(574)
 <223> n = A,T,C or G

<400> 419
 ggtacacctt tgactacagc tgcagaagtg ttcctttaga caaagttgtg acccatttta 60
 ctctggataa gggcagaaac gggtcacatt ccattatttg taaagttacc tgctgttagc 120
 tttcattatt tttgctacac tcattttatt tgnattttaa tgttttangc aacctaagaa 180
 caaatgtaaa agtaaagatg caggaaaaat gaattgcttg gtattcatta cttcatgtat 240
 atcaagcaca gcagtaaaac aaaaacccat gtatttnact tttttttagg attttttgct 300
 ttctgtgatt tttcttnttt tttgataact gcctaacatg catgtgctgt anaantnagt 360
 taaccaggga aataaccttg ngatnatggc ctanctttta gtttangtct tatgaanttt 420
 tcattgacca attctaanca ataatggttt annaacaccg tgnntnnaaa atttctggta 480
 anttgaaaat aaaaggtttn nttgaaatgg gccttttcca cnnactttnt tttnncagctn 540
 tttcttggnn aataagccct nggttctctg aacc 574

<210> 420
 <211> 573
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature

<222> (1)...(573)

<223> n = A,T,C or G

<400> 420

acctccggta	gaattcgggtg	aatccatctg	gtcctggact	ctttttgggtt	ggtaaactat	60
tgattattgc	cacaatttca	gctcctgtta	ttgggtctatt	cagagattca	acttcttctt	120
ggtttagtct	tgggagagtg	tatgtgtcga	ggaattttatc	catttcttct	agattttcta	180
gtttatttgc	gtagagggtg	ttgtagtatt	ctctgatggg	agtttgtatt	tctgtgggat	240
cgggtgggtg	atccccctta	tcatttttta	ttgngtctat	ttgattcttc	tctctttttt	300
tatntagtct	tgctagcagt	ctatcaattt	ntgtngatcc	ttttcanaaa	aaccngctc	360
ctggaattca	tttaattntt	tnaaggggtt	ttttngtggc	ctctaatttc	cttcaagttc	420
tggctctgat	ttaagttaat	atnctgggt	ttttggctac	nttttgnaan	gnggttggcn	480
cntgnntttt	ctanntcctn	ttnaantggg	gatngnttnn	aangccatt	ttnggaannt	540
tcccgccttn	ntttgggggg	catttangtt	nnn			573

<210> 421

<211> 582

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(582)

<223> n = A,T,C or G

<400> 421

ggtacgcggg	ggtccgccat	ttcgtggacg	ccgggtgagt	gagagagttg	gttgggtgttg	60
ggcccgagga	aagcgggaag	actcatcgga	gcgtgtggat	ttgagccgcc	gcatttttta	120
accctagatc	tcgaaatgca	tcgtgatttc	tgtccatttg	actgtaaggt	ttatgtaggc	180
aatcttgga	acaatggcaa	caagacggaa	ttggaacggg	cttttggcta	ctatggacca	240
ctccgaagtg	tgtgggttgn	tagaaaccca	ccngccttg	cttttgntga	atttgaagat	300
ccccgagatg	canctgatgc	aatccgagag	ctanattngn	angaacacta	tgtggcctgc	360
ccgtgtnagg	aattggaact	ggccgnaatg	gttgaaanaa	agaangttcg	aaaattcgtg	420
gnctnctntt	ccttttggrg	gtcgtcngnc	cttnagaatg	attaatcgnn	nggaaggang	480
tccttcencc	ttnncccnan	antttncant	aaangaanaa	agcttttttt	ngcaaccnng	540
aancaggtcc	cttttttttag	attgggganaa	atagnngagn	tc		582

<210> 422

<211> 570

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(570)

<223> n = A,T,C or G

<400> 422

ggtactctga	ggcttttagat	tcagtttggg	tctttggggg	ggacctctat	catcacgcct	60
ataatcatcc	cgagagtaat	catctctgga	gctccacgac	cgatcatccc	gtctgtcata	120
tcggtcttca	tagcgggtccc	cgctcctct	gtagtcatca	tccctgcgat	acctactgcc	180
aaatgctctt	ctgccactgc	ctatccggga	atcatagcct	ctatcatagt	ctctgctgcc	240
tcggtcatca	tagcgatccc	ggccaccata	tcgatccata	tcccggcgtg	ggccatccga	300

tacccatccc	gatacccatc	ccgataccgg	ctgaatcata	acgatctcga	tacttgnctc	360
caaagctatc	atcacctctt	ctaggtgggt	aagtcacaa	agctgtctgg	tagcaaggac	420
gaagcccttc	aagtctggat	ctggtttggg	cagaatnccc	atttttatca	cnggccaaaa	480
gnaacgaatc	atccctnggc	tttaaccnng	ngcttgatcn	agcaacgtcc	acntcgaaat	540
tntcctngtt	acctananaa	ctcttcattg				570

<210> 423

<211> 584

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(584)

<223> n = A,T,C or G

<400> 423

acccgggtgg	ttaaacttgc	canaatgcct	agatattatc	ctactgaaga	tttgcctnga	60
aagctgttga	nccacggcaa	aaaacccttc	agtcagcacg	tgagaaaact	gcgagccanc	120
attaccncg	ggaccattct	gatcatcctc	actggacgcc	acaggggcan	gaggtgtggt	180
tttctgaagc	agctggctag	tggcttatta	cttgtgactg	gacctctggt	cctnaatcga	240
gttctctctac	naagaacaca	ccaataaatt	tgtcattgcc	acttcaacca	anantcngat	300
atcagcaatg	taaaaatncc	aaancatctt	actgatgctt	actttaagaa	gangaagctg	360
cngaagccca	anacancnng	gaaggtgaga	tctttcgaca	canaagtatg	agaanttattg	420
agatttacgg	agcaangcan	ggattgatca	nganaagctt	ngggcctcac	caaatttttn	480
nccaanannt	tcaaagttta	tttctntnag	tttcnnnggg	cttncttgcn	antctgggggn	540
tggctttgnc	ctaattggaa	tttattnctc	ccaaaaatgg	nggn		584

<210> 424

<211> 547

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(547)

<223> n = A,T,C or G

<400> 424

actcttgggt	tgtcaatggg	actttccagc	aatccaccca	agagctcttt	atccccaaca	60
tcactgtgaa	taatagtggg	tcctatacgt	gccaaagcca	taactcagac	actggcctca	120
ataggaccac	agtcacgacg	atcacagtct	atgcagagcc	acccaaaccc	ttcatcacca	180
gcaacaactc	caaccccggt	gaggatgagg	atgctgtagc	cttaacctgt	gaacctgaga	240
ttcagaacac	aacctacctg	tgggtgggtaa	ataatcagag	cctcccgggc	agtcacaggc	300
tgcagctgtc	caatgacaac	gggaccctca	ctctactcag	tgtcacaagg	aatgatgtag	360
gaccctatga	gtgtggaatc	cagaacgaat	taagtgttga	ccacagcgac	ccagtcattc	420
tggaatgncc	tctatggnc	aaacgaaccc	caccatttcc	cctnatacac	taattaccgn	480
ccaggggtga	accttaagct	tttctggcat	gcagccttta	cccacctggc	acagtattct	540
tggctgn						547

<210> 425

<211> 567

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(567)

<223> n = A,T,C or G

<400> 425

ggtaccatcc	tttaatatagat	ctcatacaccc	agaatttcaga	tcattgaatga	ctgacagaat	60
atTTTTgttg	gcagtcctga	tttaaaacta	agactggctt	gtgggttaa	gaatatgttc	120
agTTTTtgaa	ttttaatatg	aactccaatt	cagtttatgg	tatcactgtt	taccctttt	180
aaagatatga	ttagacttcg	ttagtaattg	tcaacttttc	acaaagatgg	tgagtgccat	240
cttaaaactt	actggagatt	ggctttatat	ttagatttat	ataactgggt	atgtgaatat	300
atttaaatac	tggggaaatt	gcttcactgt	cttagaacca	agcaagattc	acctgtgttt	360
tgtgttcatg	ttcatttgcc	tcttaaaggc	aaggggtga	agataaataa	ggtagcaatg	420
tctatagttt	tggccttaac	ctatgccaat	cctaattata	attccctgga	nttnaaaang	480
gttnctttta	ccttatttgg	aanggcnttt	taaatngngg	gttnntgggn	naatatntaa	540
aggattattc	acccttttca	catnttn				567

<210> 426

<211> 563

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(563)

<223> n = A,T,C or G

<400> 426

ggtacaattt	gttcaaggaa	tttttgtaga	aaaatacgat	cctacgatag	aagattctta	60
tagaaagcaa	gttgaagtag	atgcacaaca	gtgtatgctt	gaaatcttgg	atactgcagg	120
aacggagcaa	tttacagcaa	tgagggattt	atacatgaaa	aatggacaag	gatttgcatt	180
agtttattcc	atcacagcac	agtccacatt	taacgattta	caagacctga	gagaacagat	240
tcttcgagtt	aaagacactg	atgatgttcc	aatgattctt	gttggttaata	agtgtgactt	300
ggaagatgaa	agagttgtag	ggaaggaaca	aggtcaaaat	ctagcaagac	aatggaacaa	360
ctgtgcattc	ttagaatctt	ctgnaaaatc	aaaaataaat	ggtaatgaga	atTTTTtatg	420
acctantgcg	gcaaattacc	ggaaaaactt	ccngngcctg	ggaaggctng	gcaaaaaggcc	480
ttcatgggtca	gntgcttaat	tatnctaaat	gccntgganc	ttttgaccag	gntctgaana	540
actgttgnc	aattcaacag	ggg				563

<210> 427

<211> 567

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(567)

<223> n = A,T,C or G

<400> 427

ggtacttttt	tttttttttt	tttttttttt	tttttgtaa	aaaccataca	tcctttttat	60
------------	------------	------------	-----------	------------	------------	----

tgntaagtc	taaagaggt	tcaaaattaa	aagcaaaaat	tacagggt	gacttaacaa	120
aactactagg	agcgtcaaag	gaagtgaaaa	tggtactagg	cgcggggcaa	tatgaattaa	180
tgaacatggg	aaggacaagg	atgggganaa	cggtgagcat	gtgctgaana	tactagggga	240
gaggatctgg	tgaaaaattt	gatcttanac	aagcgcttag	gtaaagaaat	aatgggataa	300
gatttctaaa	ccccactatg	gagcttaaga	gtcatcctng	ccattggcgc	tgtctctgnc	360
atcctctcct	tcctcaagnc	tctttttcat	catnctttga	tccaattcca	gctgggcaat	420
tccccgcgac	tttnattatc	atcatcattc	cantanggnn	ccntttctta	ggaannngtn	480
ttttggnccc	cccttaanat	ttcaatttcc	cttnnnccca	ttttttttan	ggagnttggt	540
gcnnatggccc	ttttnggntt	aaaaatn				567

<210> 428

<211> 578

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(578)

<223> n = A,T,C or G

<400> 428

ggtaccctat	gaacctgact	ctgtgggtcat	ggcagaagct	cctcctgggg	tagagacaga	60
tcttattgat	gttggatnca	cagatgatgt	gaagaaagga	ggccctggaa	gaggaggag	120
tggtggcttc	acagcaccag	ttggtggacc	tgatggaacg	gtgccaatgc	ccatgcccat	180
gcccattgct	atgccatctg	naaatacngc	ctttctcata	tccactgcca	aaggggaccat	240
canatttcaa	tggactgcca	atggggacct	atcaggcctt	tnccaatatt	catccacctt	300
cagataccag	cnactcccc	atcgatgaa	tctgnaatg	acattaatgc	tgataatgaa	360
tatctctttn	tgcacanatt	gttgggtcctg	gacccagcc	aanaancctt	tgcaaanctt	420
nctttccaga	cctggaggat	tacttatnga	caccnttgct	cctaaccaga	agttgnccat	480
ttgngcccng	aacancactt	tcccaactgg	canttnngctg	gatcccaggn	ccttcnggat	540
ttggaanaac	nttggctttt	gatggatttt	ttccccgg			578

<210> 429

<211> 572

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(572)

<223> n = A,T,C or G

<400> 429

ggtaccaaga	gtttgctcct	ggctgctttg	atgtcagtg	tgctactcca	cctctgcccc	60
gaatcagaag	cagcaagcaa	ctttgactgc	tgtcttggt	acacagaccg	tattcttcat	120
cctaaattta	ttgtgggctt	cacacggcag	ctggccaatg	aaggctgtga	catcaatgct	180
atcatctttc	acacaaaaga	aaagtgtgt	gtgtgcgcaa	atccaaaaca	gacttgggtg	240
aaatatattg	tgcgtctcct	cagtaaaaaa	gtnaagaaca	tgtaaaaact	gtggcttttt	300
ctggaatgga	attggacata	gcccangaac	agaaagaacc	ttgctgggct	ggaggtttca	360
cttgacatc	atggaaggg	ttagtgctta	atctaatttg	ggcctcactg	gacttngncc	420
atttaatgaa	gttnantcat	tattgnnata	atagtttgct	ttgtttnaan	ccttnncatt	480
taaagttaaa	actggaattt	nanngtaatt	tnaacttgta	nggtttcctg	ggtttagctt	540
tttaaactnt	aattttttcca	taagcnnntt	tg			572

<210> 430
 <211> 591
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1) ... (591)
 <223> n = A,T,C or G

<400> 430
 ggtacagccc aggtaatTTg ctgagcctaa tgggtgtcag ggtcagtcta agtgaaggca 60
 aagagaggct gggatgaagg gtgcaaagga atagtaaaga aagcatgttt gagatccana 120
 acagaataat gggtagtaga gggagggtatt gaggatagaa nagtatatgg gtttggcacc 180
 acgggggtgga taggcaaaac atttggttga taangcgcag attctgaact aacttgtaag 240
 gcttgtctgg ttttaggaca ggtaaaatgg nggaatggta aggagaagtt tataggtttt 300
 atgagcccat gctgtancan gcaagtgata actngctttt aatccctttt cnaaagcaat 360
 gcctggngnt atgaagnata tttggcattt gatcnggggt tnaangngntg attagngttn 420
 ctantgaaca atngnaaagg ggntgccatg atcngtnncc caaggatgng attttanggn 480
 antctentac ttgtgggggt naaggggtggn gggntttttac naggnggggt cccnaagggg 540
 gcctnttggg tntangnaat aaanggccng nnaatngana atccnnnttn n 591

<210> 431
 <211> 565
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1) ... (565)
 <223> n = A,T,C or G

<400> 431
 accagtgatg ttttgataga agcatataat gtttaatgat caagtcagga taaatgggggt 60
 atccatcacc tcaagcacat ataatcattt ctttgtatta ggcattattca aattccactc 120
 ttttagttat ttttaaataat ccagtaaatt agatcttatt cattctatct agatgtattt 180
 ttgtacttta tttttctcaa atatttttac ttatgctttt tgtcattatc cacagtgttt 240
 ttttttaaag cctgagccac tttgtgggtt cagcctcaat ataataatca tccccttact 300
 cttagactaa ttcccttttcc cctgncactt tgctgtata ctctgtaaaa atgangacct 360
 tagaaaatca acatttcctg gtgaactttg agagactatt acaagcagtg cccaaaacag 420
 tangaataag gcaggtaaaa ccagttggga tagccagatn tattattgat ctggtnggga 480
 aaanggataa nttggngggc atgggtttcca nggcantcgn gaattcccca ttagctttta 540
 gggtcnatnn angntggccc anggg 565

<210> 432
 <211> 578
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1) ... (578)

<223> n = A,T,C or G

<400> 432

acgcgggggc	caccgtggag	agcagagcgc	ggcgggctgga	agctgctaag	tcagagccgc	60
gatgttccgg	attgagggcc	tcgcaccgaa	gctggacccg	gaggagatga	aacggaagat	120
gcgcgaggat	atgatctcct	ccatacggaa	ctttctcatc	tacgtggccc	tcctgcgagt	180
cactccattt	atcttaaaga	aattggacag	catatgaaga	caggacatca	catatgaatg	240
caccgatatg	aagagcctgg	ttacagtttc	gactcctctc	tgnaagtga	taggccaga	300
aagggtgaag	agactctttg	aatggacata	aaattctgct	tgtnnagaac	caagttttgg	360
ntctgggtna	ctgacctttc	aaaagctaaa	attttaaaac	tattttgggg	aagtttttta	420
tttnntatt	nntcngtttn	tnataaaaa	agtaccttgg	tnccggnacc	accnttaag	480
ggccnaattn	cagncnnt	ngngggcgn	ttactttng	ggatnntaa	nttcggganc	540
cnaancttgg	ggggtaantc	angggtcata	nnetggtt			578

<210> 433

<211> 563

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(563)

<223> n = A,T,C or G

<400> 433

acttcttctg	gccaaaggct	gttccacatt	cactacattt	aaaaggcttc	tctccaatat	60
ggattttctc	atgctcagta	aggttggatt	tgccactgaa	ggtttttcca	cactccttac	120
atacaaaggg	cttctctcct	gtgtgagttc	tctgggtgct	gatgaggttt	gacttctgaa	180
tgaaagcttt	cccgaatct	ttacactcaa	aaggtttttc	tccagtgtga	attttctggt	240
gcgtaaggag	gttttcttct	tggttaaatg	attttccaca	ttcattacat	tcgaaaagct	300
tctcgccagt	atgggtgttc	tgatgtttta	tgacatactg	cttttggtta	aaggcttttc	360
cacactcggt	acattcaaaa	gggttctctc	tccgtgtgaa	aatgctcatg	ctcantgang	420
tttgaattgn	nggcttgaac	acttttccca	tacccttaca	ggcaaanggg	gttttcccn	480
ttggaanatn	tntggctgcn	tnaagntggt	gacatctgga	tnggaaacct	tttcncatt	540
tccaaagggn	tttttttcnn	nag				563

<210> 434

<211> 563

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(563)

<223> n = A,T,C or G

<400> 434

ggtacagctg	tctgcattga	aaattcatgc	atggagaaaag	ggagtaagca	agggagaaac	60
ggtgcgattc	acatattccg	cgagatcatc	aagccagcag	agaaatccct	ccatgaaaag	120
ttaaaacaag	ataagcgctt	tagcaccttc	ctcagcctac	ttgaagctgc	agacttgaaa	180
gagctcctga	cacaacctgg	agactggaca	ttatttgtgc	caaccaatga	tgcttttaag	240
ggaatgacta	gtgaagaaaa	agaaattctg	atcgggacaa	aaatgctctt	caaaacatca	300
ttctttatca	cctgacacca	ggagttttca	ttggaaaagg	atttgaacct	ggtgttacta	360

```

acatttttaa gaccacacaa ggaaacaaaa tcttttcttg aaagaaagta aatngatcca      420
cttctgggtga atgaatttga aattcaaagg aatctggcct tcatgccanc aaatgggggt      480
aattcatgnt ggagaataac ctcttttata cagccgnaca cacctgttgg aaatggatcc      540
aactgctgga aattncttaa taa                                     563

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```

<210> 435
<211> 558
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(558)
<223> n = A,T,C or G

```

```

<400> 435
ggtacgcggg ggaagatggc ggccgtgcag gcggccgagg tgaaagtgga tggcagcgag      60
ccgaaactga gcaagaatga gctgaagaga cgctgaaag ctgagaagaa agtagcagag      120
aaggaggcca aacagaaaga gctcagttag aaacagctaa gccaaagccac tgctgctgcc      180
accaaccaca ccactgataa tgggtgtgggt cctgaggaag agagcgtgga cccaaatcaa      240
tactacaaaa tccgcagtca agcaattcat cagctgaagg tcaatgggga agaccatac      300
ccacacaagt tccatgtaga catctcactc actgacttca tccaaaaata taagtcacct      360
gcagcctggg gatcacctga ctgacatcac cttaaagggt gcaggtagga tccttccaaa      420
agancttntg ggggaaactn antcttctnt tgaactttca aggaaanggg tgaagtttgc      480
agtcatgggc caattccaga aattttaaat cagnagaaga atttttccta ttaataccaa      540
ctgggtcggg ggagactn                                     558

```

```

<210> 436
<211> 528
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(528)
<223> n = A,T,C or G

```

```

<400> 436
ggtacaaaaa aaacchata taaattaaga atgaatacat ttacaggcgt aaatgcaaac      60
cgcttccaac tcaaagcaag taacagccca cgatgttctg gccaaagaca tcagctaaga      120
aaggaaactg ggtcctacgg cttggacttt ccaaccctga cagaccgcga agacaaaaca      180
actggttctt gccagcctct agagaaatcc cagaaacactc agccctgaca cgттаатacc      240
aaggggaaca gttaactcca atacaaggtc aaaatcagca acaagttcta caatccagtg      300
ctgatatcag atacaaagct tcaagggcaa tttcttttcg aaggcttatt ccagtttcgt      360
gaggctagca tgaagtgtgt gcatttgcca ggggcaaat tctattctca attaaccat      420
gcagcaaant gctacgcata tggctgagtc cggtttanaa nccatttgcc ggnggaccaa      480
tggaaggggc ccgaattcgt cnnaacttgn cccgggcggg ccgttcaa      528

```

```

<210> 437
<211> 576
<212> DNA
<213> Homo sapiens

```

<220>
 <221> misc_feature
 <222> (1)...(576)
 <223> n = A,T,C or G

<400> 437
 acttttttttt tttttttttt tttttttttt aggtttgagg gggaatgctg ganattgtaa 60
 tgggtatgga gacatgtcat ataagtaatg ctagggtgag tggtaggaag ttttttcata 120
 ggaggtgtat ggggttggtcg tagcggaatc ggggggtatgc tgttcgaatt cataagaaca 180
 gggaggttag aantagggtc ttggtgacaa aatatgttgt gtagagttca gggganagtg 240
 cgtcatangt tgttcctagg aanattgtac nggtcagggt tgtttattat aataatgtn 300
 ggggtatccgg ctntgaaana atngggccaa ngggcctgag gtgtattcga ngttnaaacc 360
 tgagactagt tcggactccc ntttgcaagg ncccaaagggt ggttnggttt ggcccttgct 420
 annngtgnga naataaatcn tntttattgg cccaagggtt cttaacngcn aggagtnaat 480
 ccaaaggggt ncntnggntt ttnnnanaaa nggttgnaaa aagggttaaag ggaccncct 540
 ttntnntaa tgntcgnaat gtcaaatinga tngcnn 576

<210> 438
 <211> 576
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(576)
 <223> n = A,T,C or G

<400> 438
 ggtaccccaa ttaccagtat ggtggaccct accccttctt ctctgcattg ggaaacagaa 60
 cagagaacag aaaaaatcat tccatcttgc tcttaactct tccacctat gtgctcagtt 120
 tttcaagtag aatttctatt cctttgctgg tgcttttggg tttttccaat gtaggaatca 180
 agcttttcag tgcagctttg actttgtttg caacttccag gtcacaactc tggaggaggc 240
 tagaaagaat aatggcacct cgatttacac tagcccagga cttcagggtc ttcataccaa 300
 catgctctac aagtgttttt gcaaaaacaac cttctcttcc attntctttt catcttttta 360
 tcttgctcta ttaaccactt nagaaactaa gaatgtccct gcaaggatgt tctggcaatg 420
 ntgaaagctt ctccgtcctt ggccaccagg atgcaagtcc ntggttnttg ccagcttggc 480
 cnatnggcat tccatnggna nggcttgaac cgttttccag ggggcagant cccaaaatgg 540
 ccngacacca acccnacang cagacttntt ttagcn 576

<210> 439
 <211> 578
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(578)
 <223> n = A,T,C or G

<400> 439
 cgaggtacgc gggggagaaa aaacctgcgg aaaatggtag cgatggcggc tgggcccaggt 60
 ggggtgtctg tgccggcggt tgggctacgg ttgttggttg cgactgtgct tcaagcgggtg 120
 tctgcttttg gggcagagtt ttcacgagag gcacgcagag agttaggctt ttctagcaac 180

```

ttgcttttga gctcttgtga tcttctcgga cagttcaacc tgcttcagct ggatcctgat 240
tgcagaggat gctgtcagga ggaagcaciaa tttgaaacca aaaagctgta tgcaggagct 300
attcttgaag tttgnggatg aaaattggga aggttccctn aagtccaanc ttttgttang 360
agtgataaaa cccaaactgt tcagaaggac tgccaaatna aagtatgtnn cgtgggttca 420
aacntgaat taaaaggctt ttngaccaac atngggnaa attgcttgan nacttgtcca 480
tttcttaaaa ttgggaacnc tggaccnggt nanaaanatt tcnngattgga aaantttgga 540
ccncatttta aatcttgcct aaattttggc caatcctt 578

```

<210> 440
 <211> 573
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(573)
 <223> n = A,T,C or G

```

<400> 440
ggtacttttt tttttttttg agacaggggc ttgccctgtc acccaggctc gagtgcactg 60
gagtgatcac agctcactgg cctcaagtga tctcctgcc ttggcccctt aagtgccagg 120
gttacaggca tgagctacca tgccctggcag aaattcaaga tttggataaa cttacttctt 180
tgccaagcct gttcttcaag ttattcagaa ctgggtgtat accttgcct catatgtatc 240
ttgtccctgc tgtcttttag gtttagcaagg tgtatgaata cttttaagtt ttgtttgttc 300
ttttcctcgt ggtatcaagt gaaatactga tctattctct ggctaggggc aatttacaaa 360
attgccatgg aactgagcca aaaggcccca cgtgggataa aaattnctta ccatcgacgc 420
ccanccgtan tttttcaagg tattggcttt tggaagnttt accaaatttc nggtaaacca 480
aaattcnaaa agnaaaaaat tnccttgng taaccttgcc cgggcggccg ttcaaaaagg 540
cnaatttcca ncacattggg cggccgttaa tna 573

```

<210> 441
 <211> 572
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(572)
 <223> n = A,T,C or G

```

<400> 441
ggtacaaaat tttattaaag gtcttttagag agcaacatcc agactccaga atacagctgc 60
caaggagacc ctgttatgct gtgggggactg gctggggcat ggcaggcggc tctggcttcc 120
cacccttctg ttctgagatg ggggtgggtg gcagtatctc atctttgggt tccacaatgc 180
tcacgtggtc aggcaggggc ttcttagggc caatcttacc agttgggtcc cagggcagca 240
tgatcttcac cttgatgccc agcacaccct gtctgagcaa cacgtggcgc acagcagtgt 300
caacgtagta gttaacaggg gtctccgctt gtggatcatc aagccatcca caaacttcat 360
ggatttagcc ctctgncctt cggaggttcc cagacaccca caanctngca agcctttggc 420
cccacttttc catgatgaaa ctgnagnac aaccatangc aagggccctt cggacannta 480
aggccttcc aaggagnttg naacnana naacttttgc ttgggcantg ggcacaccag 540
nacntnaag nggccccctt ttaagcata aa 572

```

<210> 442

<211> 562
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1) ... (562)
 <223> n = A,T,C or G

<400> 442
 acaggtcaga gtcttctttt cttttctttt tgagatggag tcttgctctg ttgccagact 60
 ggagtgcagt ggtgcgatct gggctcactg caatctccac ctcccgggtt caagcgattc 120
 tcttgccctca gcctcccgag taactgggac tacaggtgcg cgccaccaag cccagctcat 180
 ttttgatatt ttagtagaga tggggtttca cgatgttggc taggatggtc tcgatctctg 240
 gtcagagtct tttctgtaaa tatccttggt aaagaagcaa ttttagactg tagctgttgc 300
 aaatgcttta aggaagaagc aaaacaactg tcaagtcttc ctgaaatgaa gaaactncac 360
 cagggctgct atatcagaac aaccncaacc aagcacttca aacatgatgc cgacaggtgg 420
 ccccagctta aaaaaccagg aanaagtten gantccnnaa actgngaatt cctcttggtg 480
 ttttggaatt aattgggggc cagtagccaa gttatnagac caaatcangg cntagggccc 540
 cgtattattt ggcggggatt tg 562

<210> 443
 <211> 585
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1) ... (585)
 <223> n = A,T,C or G

<400> 443
 actttttatt tttggtggtg aaattgactg atgattttcc tttttcttcg ctggactatt 60
 gtgccaactg ccaggctgcc tcttgccctt acagccctaa gtggctgctt tctttccatc 120
 aactcccaac ttcttctgt gaagtttaat tgtctcaacg cctccccctc ccccatcccc 180
 tccatttttc tcccaagaaa cctgactcaa ttatttgcatt attttgagaa actgctgcag 240
 attagtctct tttgccagtt ttccctggaa ctctggcct tttgtggagg ggagggatgg 300
 agagaatagg aatcttcact agaagccgtg ggaagaattg gaagttacat gctgtatatg 360
 caatgtccag cagtctgata aactgacgat tcttaataca gattttttcc tgatggggaa 420
 gggactttta ttttctttta nagaggggaa agtgtgagct cttcccttat tcctaattggc 480
 tatttttgaa gcaanaagg ccacaacatt ngcacatgcc acctgcnaag gaccttgagt 540
 nagtgaagnc tcctaaaact gggttaanaa ccttgttttc tctnn 585

<210> 444
 <211> 437
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1) ... (437)
 <223> n = A,T,C or G

```

<400> 444
acgcgggggac gtgactcagc acttttcccca gagcccggac tgcggagaac aatatacctcc      60
tcctaacag ataaacagcc cttgttcctc gggataagga ctggcagtec cctgacaccc      120
taagaccggc atctgtcgat gttatttccc cagcatggcc gaaacagaag ccctgtcgaa      180
gcttcgggaa gacttcagga tgcagaataa atccgtcttt attttgggcg ccagcggaga      240
aaccggcaga gtgctcttaa aggaaatcct ggagcagggc ctgttttcca aagtcacgct      300
cattggccgg aggaagctca ccttcgacga ggaagcttat aaaaatgtga atcaagaagt      360
ggtggacttt gaaaagttgg atgactacgc ctctgccttt caaggtcatg atgttggatt      420
ctgtgcctgg gtacctn                                     437

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```

<210> 445
<211> 592
<212> DNA
<213> Homo sapiens

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<220>
<221> misc_feature
<222> (1)...(592)
<223> n = A,T,C or G

```

```

<400> 445
actttttttt tttttttttt tttttttttt taaggtttga gggggaatgc tggagattgt      60
aatgggtatg gagacatatc atataagtaa tgctaggggtg agtggtagga agtttttttca      120
taggaggtgt atganttgnn cgtagcggaa tcgggggtat gctgttcgaa ttcataagaa      180
cagggagggtt aaaagtaggg tcttggtgac aaaatatgtt gtgtanagtt caggggaaag      240
tgcgtcatat gttgttccta ggaanattgt antggtgagg gtgttaatta taataatggt      300
tgtgtattcg gctatnaana atagggccaa atgggcctgc ngcctattcn atgtttaanc      360
tgagacttnt tcggactccc cttcggcaan gtcnaantgg ggttcggttg ngcncctgcag      420
tgnggagata nntcntntta ntggccaatg gttnngatgg ccagaataat cannanggnt      480
tcntntntcn tnaaaagggtc naaatggttn angganaccn cttattagga attgttaatc      540
ttnaatgatn gttntggnga cncatatagg anaatgtnag gnctactccn ng                    592

```

```

<210> 446
<211> 599
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(599)
<223> n = A,T,C or G

```

```

<400> 446
ggtacggcaa acacaacgga cctgagcact ggcataagga cttccccatt gccaggggag      60
agcgccagtc ccctgttgac atcgacactc atacagccaa gtatgaccct tcctgaagc      120
ccctgtctgt ttcctatgat caagcaactt ccctgaggat cctcaacaat ggtcatgctt      180
tcaacgtgga gtttgatgac tctcaggaca aagcagtgtc caaggaggga cccctggatg      240
gcacttacag attgattcag tttcactttc actgggggttc acttgatgga caaggttcat      300
agcatactgt ggataaaaag aaatatgctg cagaacttca cttggttcac tggaacacca      360
aatatgggga ttttgggaaa gctgtgcagc aacctgatgg actggccgtt ctaggtattt      420
tttttgaagg ttggcagcgc taaaccnggc ctnataaag ttgttgaatg tgctggattc      480
cattaaaaca aagggcaaga attgctgact ttcactaatt nnaatcctcg tnggccttct      540
tcctgaaatc cttggattac cggacctncc cagcttactn accanccttc tcttttngg      599

```

<210> 447
 <211> 588
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(588)
 <223> n = A,T,C or G

<400> 447
 ggtacgcggg atgagtgtgg aatccagaac aaattaagtg ttgaccacag cgacccagtc 60
 atcctgaatg tcctctatgg cccagacgac cccaccattt cccctcata cacctattac 120
 cgtccagggg tgaacctcag cctctcctgc catgcagcct ctaacccacc tgcacagtat 180
 tcttggtgta ttgatgggaa catccagcaa cacacacaag agctctttat ctccaacatc 240
 actgagaaga acagcggact ctatacctgc caggccaata actcagccag tggccacagc 300
 aggactacag tcaagacaat cacagtctct gcggagctgc caagccctcc atctccagca 360
 acaactccaa acccgtggag gacaaggatg ctgtggcctt ccctgtgaac ctgaggctca 420
 gaacacaacc tacctgtggg gggtaaatgg tcagagcctc cagcagtcct aaggctggag 480
 ctgtccaatg gcaacangga cctnactcta ttcaatgtca caagaaatga cncaagaacc 540
 tatgnatgtg gaatccagaa ctnagtgtat caaacccaat gaccagnn 588

<210> 448
 <211> 593
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(593)
 <223> n = A,T,C or G

<400> 448
 accatttgtc tgacctctgt aaaaaatgtg atcctacaga agtggagctg gataatcaga 60
 tagttactgc taccagagc aatatctgtg atgaagacag tgctacagag acctgctaca 120
 cttatgacag aaacaagtgc tacacagctg tgggtccact cgtatatggt ggtgagacca 180
 aaatggtgga aacagcctta accccagatg cctgctatcc tgactaattt aagtcattgc 240
 tgactgcata gctctttttc ttgagaggct ctccattttg attcanaaaag ttagcatatt 300
 tattaccaat gaatttgaaa ccagggtctt tttttttttt ttgggtgatg taaaacncaa 360
 ctncctgnca ncaaaataat taaaatagnc acattgntat cttttattag gtaattcact 420
 tcttaattan atggntcaat actctaagna tcaaaatntt ccaattatna tggctcacct 480
 gaaagaagna tgctctttta aggaatacag cttcttcnat tnacaattta acanggggag 540
 aaaattaaan tnaangantt ganatctgga gngtannaa ngntctcgcn ttc 593

<210> 449
 <211> 577
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(577)

<223> n = A,T,C or G

<400> 449

actgtgggtc	gaagtaatgg	atacggacgt	aaccatcttc	gccgccgctg	ctgtagctct	60
tgccatcagg	atggaaggca	acactgttga	taggtccaaa	gtgacccttg	actcttccaa	120
actcttcttc	aaaggccaaa	tggaagaacc	tggcctcaaa	cttgccaatc	ctgggtggagg	180
ttgtgggttac	atccatggct	tccctgaccac	cgcccaggac	cacatgggtca	tagttggggg	240
agagggcagc	tgagttgaca	ggacgttctg	tccggaaagt	cttctgatgt	tcaagagttg	300
tggagtcaaa	aagcttggct	gtgttgtcct	tggacnccgc	acaaacatgg	tcatgtccct	360
ggataactgg	atgtcgttga	tctgccggga	gtgctcctta	acattcacca	acacctcttc	420
anacttggca	ctatactggg	tgactctcca	ctcttatggc	cnggatgatg	cactcccca	480
aggggtacca	aacagnactg	gtgatttaga	atcattgcan	ggatcttatg	tagggctcat	540
tgntgcaatc	tggcttggat	ccgcagtcga	aaaagnt			577

<210> 450

<211> 575

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1) ... (575)

<223> n = A,T,C or G

<400> 450

ggtacttgtg	atcacactac	gggaatctct	gtggtatata	cctggggcca	ttctaggctc	60
tttcaagtga	cttttggaaa	tcaacccttt	ttatttgggg	gggaggatgg	ggaaaagagc	120
tgagagttta	tgctgaaatg	gattttataga	atatttgtaa	atctattttt	agtgtttgtt	180
cgttttttta	actgttcatt	cctttgtgca	gagtgtatat	ctctgcctgg	gcaagagtgt	240
ggaggtgccg	aggtgtcttc	attctctcgc	acatttccac	agcacctgct	aagtttgtat	300
ttaatggttt	ttgtttttgt	ttttgtttgt	ttcttgaaaa	tgagagaaga	gccggagaga	360
tgatttttat	taattntnt	tttttttttt	tactatttat	agcttttaaaa	agggcctncc	420
ttccctctct	ctttctttgg	nccttttcat	taacccttcc	ccagtttttt	ttactttaaa	480
ccccgttctc	atggcctnng	ccttttgaag	cgnttctctc	tataaaaagc	tttgccgaac	540
aanttttttt	taccgatccc	aaatttatga	agggg			575

<210> 451

<211> 573

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1) ... (573)

<223> n = A,T,C or G

<400> 451

actaggctaa	ctagaaggat	ctcatcccca	tatgtggtct	catttcaagt	ctatggatga	60
ctaccttcat	tgctgtgtgc	gagatgggtt	cacccttga	aaatatgggc	acttcagcat	120
aaaatagtta	aatctttata	atgatcaatt	cactctacct	ccttttacat	gcagctgaaa	180
aatgacaggc	tagggacata	gaatattgtg	aactttatac	tgtagaatac	actgtccatt	240
aatgatcac	tagctaattg	tcactaaaatt	tacaaattaa	ggaaattata	tatagaatac	300
tgcaaaaaca	cagtaaaaag	actgaagttc	gccattttct	gctcaggaag	tctcttcact	360

```

cctaagcttc atatgttgcc ttctggcttc aaaattctgc tattattact gttttcctcc 420
tttgatcttc ctttggctcc cagtgccaga cttccaagcc ttttngttaa aaagccatct 480
tttggatgcc atttcnaaca gcttcagtga tgcctctgaa aaaaggatct gccggctaen 540
atttctcngg ttcgtgcttc ctaccgganc tcc 573

```

```

<210> 452
<211> 595
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(595)
<223> n = A,T,C or G

```

```

<400> 452
acaattttat ccctaaaaact ctgttgacat caaaatatga cagttgctat atccataaaa 60
tattttacata gcacggcata ttaagcttta gacacttggc aattaaacca cataaaaaga 120
ggacaagacc cccatcctac atgtttggaa tcagggtgttc accggtcctt atctggcgac 180
tgtacgcggg tggggtcctt acttgtattc tgttatcagc tgattttgaa acatataata 240
atgattttct tgttcccttc tttaactagc tgcctttaga ttttgataat cacagtctta 300
aaatactagg aaagaagtgg atgggaattg taggcataga ttcatatca agggcatttc 360
aagacagaat ttttaattcc tgtagtaggc ttgctggagc naaaggaaaa tgtgctgggt 420
aaaaatcaac ttatgccatt ttaaaatttg ataaaatttg gagtggcatn ctgctaaggg 480
gagaccttgg gccggacccc cttangggca aattccngca cactgggggg cgggtactang 540
gggatccgac ntcggnccan acttggcgna tcatgggctt antgttcctt gnggn 595

```

```

<210> 453
<211> 380
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(380)
<223> n = A,T,C or G

```

```

<400> 453
ggtacgcggg gagccgcctg gataccgcag ctaggaataa tggaatagga ccgcggttct 60
attttgttgg ttttcggaac tgaggccatg attaaagagg acggccgggg gcattcgtat 120
tgcgccgcta gaggtgaaat tcttggaccg gcgcaagacg gaccagagcg aaagcatttg 180
ccaagaatgt tttcattaat caagaacgaa agtcggaggt tcgaagacga tcagataccg 240
tcgtagttcc gaccataaac gatgccgacc gccgatgcgg cggcgttatt cccatgacct 300
gccgggcagc ttccgggaaa ccaaagtctt tgggttccgg ggggagtatg gttgcaaaaa 360
aaaaaannaa aaaaaaaagt 380

```

```

<210> 454
<211> 589
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature

```

<222> (1)...(589)

<223> n = A,T,C or G

<400> 454

ggtactcttg	gtttatcaat	gggacgttcc	agcaatccac	acaagagctc	tttatcccca	60
acatcactgt	gaataatagc	ggatcctata	tgtgccaaagc	ccataactca	gccactggcc	120
tcaataggac	cacagtcacg	atgatcacag	tctctggaag	tgctcctgtc	ctctcagctg	180
tggccaccgt	cggcatcacg	attggagtg	tggccagggt	ggctctgata	tagcagccct	240
ggtgtatttt	cgatatttca	ggaagactgg	cagattggac	cagaccctga	attcttctag	300
ctcctccaat	cccattttat	cccatggaac	cactaaaaac	aaggtctgct	ctgctcctga	360
agccctatat	gctggagatg	gacaactcaa	tgaaaattta	aagggaaaac	cctcaggcct	420
gangtggtgtg	ttactcagag	acttcaccta	actagagaca	gtcaaactgc	aaccatgggt	480
gagaaattga	cgacttcaca	ctatggacag	cttttnccaa	gatgtcaaac	aagactcctc	540
atcatgataa	ggntcttacc	cctttaattg	nccttggtat	gcctgcctc		589

<210> 455

<211> 589

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(589)

<223> n = A,T,C or G

<400> 455

ggtacgcgga	agagacaggg	tttcaccatg	ttgccagggc	tggtttcgaa	ctcctgacct	60
caggtgatcc	accgcctcgc	gcctcccaaa	gtgctgggat	tacaggcttg	agccccgcgc	120
cccagccatc	aaaatgcttt	ttatttctgc	atatgttgaa	tactttttac	aattcaaaaa	180
aatgatctgt	tttgaaggca	aaattgcaaa	tcttgaaatt	aagaaggcaa	aaatgtaaaag	240
gagtcaaaac	tataaatcaa	gtatttgga	agtgaagact	ggaagcta	ttgcattaaa	300
ttcacaaaact	tttatactct	ttctgtatat	acattttttt	tctttaaaaa	acaactatgg	360
atcagaatag	ccacatttag	aacacttttt	gttatcaagt	caatattttt	agatagttag	420
aacctggtct	taagcctaaa	agtgggcttg	attctgcagt	aaatcnttta	caactgcctc	480
gacacacatt	aaccttttta	aaaatngacc	ttcccgaagt	cttttggtag	catggnacac	540
ctgatgctta	natgttcang	taattaatat	ggnccagnag	tnttgttnc		589

<210> 456

<211> 582

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(582)

<223> n = A,T,C or G

<400> 456

acagaatggt	gatacaaagc	ttaaaattct	tgcatatggt	catagaaaat	gcattcttgg	60
ttttgtgttt	ttatcacttg	cttccaactt	aggcttttgg	ctcagaagat	tattgaataa	120
tgatttgtct	tagtttctgt	ttcagtaagg	gaattctgag	gccgttgcta	tgataccatc	180
attaagacat	tcacatgtct	tcatataata	tctcttcatt	tcaaataccta	atcactattt	240
catactatta	cagggctttg	atgctgccag	cactgtcttt	tacataggaa	attctagatt	300

tgcacagtaa	tagaggaatt	agaagtacct	aactatacac	tttgattcag	cctgctaaat	360
caggggttca	atactagctt	ggacaaactt	tgtaagtaat	taattgctac	cagccttatt	420
ggaaacaaat	tatcaactag	tttcccttgc	caatttttga	aattcactgn	ttcacttaat	480
ctatttatatt	actaataatg	gattaataaa	gatgaattaa	ttattattac	ttactagtnt	540
aaatgaaaaa	cagggactga	aatagtctgn	atccgngttg	ca		582

<210> 457
 <211> 380
 <212> DNA
 <213> Homo sapiens

<400> 457						
ggtacttttt	tttttttttt	tttttggagt	tttttagttta	ttaatgttct	tgcgaaaaat	60
ccacagtggc	cacagctaac	atcattgcag	cacctttact	ccttcggctg	tgatccaatc	120
tccagctcac	ttctttttgc	cagcaccaac	attggccttt	gcagtcctcc	tgactttctt	180
cattctgttc	ttgcgttctt	ttcgttgctt	tcttgaggtc	tttttcttct	catacaggcc	240
atgtcttgca	agtctatgtt	tgggttcatt	tttctttgca	taatccaggg	aatcataaat	300
catgccaaag	ccagttgtct	tgccaccacc	aaaatgagtt	ctgaatccaa	atacaaagat	360
gacatccggt	gtggtcttgt					380

<210> 458
 <211> 382
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(382)
 <223> n = A,T,C or G

<400> 458						
acgcggggag	aacagccacc	cctctctcgg	gcactgctgc	catgaatgcc	ttcctgctct	60
ccgcactgtg	cctccttggg	gcctggggcg	ccttggcagg	aggggtcacc	gtgcaggatg	120
gaaattttct	cttttctctg	gagtcagtga	agaagctcaa	agacctccag	gagccccagg	180
agcccagggt	tgggaaactc	aggaactttg	cacctatccc	tggatgaacct	gtgggtccca	240
tcctctgtag	caaccgaac	tttccagaag	aactcaagcc	tctctgcaag	gagcccaatg	300
cccaggagat	acttcagagg	ctggaggaaa	tcgctgagga	cccgggcaca	tgtgaaatct	360
gtgctacgc	tgctgtacc	tn				382

<210> 459
 <211> 592
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(592)
 <223> n = A,T,C or G

<400> 459						
ggtactgagg	aaatattttg	taaagtgagc	tttgggtata	acttagcccc	atcattatth	60
agagaataga	ggaggaagaa	agaggaagga	ttttaaaggc	agacaatgac	agaccattca	120
ggataggtag	ggtttttaaag	ggagataaac	acagtctcat	caactaagga	gagatttgct	180

```

gcagtaaata ggatgagggga aatagtctgt gggatgcaag caaaggaagc aggggtgcctt      240
agacactgag tggagccaga aagatcatgc ggcctttttc caagtacatg gccaccaagt      300
aagaatgggtt ggtgacaaga cagaaggcta aaacaggaag gtaatcttgt gcacctgaca      360
aatngaaaga attaaggatc aaaattgaag caggctntaa gaggttcaag aaattcttaa      420
aaccctaaaag tgatttggaa gccccaaact ttccggtaat gctncccatg gcatgatggg      480
ccaaaacctt ggggggttctt aagtttnaaa agccctntnc caaattttta tggacccctt      540
acattttttc taatcaatcc cccctttcca aaaaaatngg acctcntttt tt              592

```

<210> 460
 <211> 578
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(578)
 <223> n = A,T,C or G

```

<400> 460
acgcggggcac tatcctgaat tatgtgcctg tctagataag cagagaccat gccaaagcta      60
taatggaaaa caagtttaca aagagacctg tattttctttc ataaaagact tcttggcaaa      120
aaatttgatt atagtatttg gaatagcatt tggactggca gttattgaga tactgggttt      180
gggtgttttct atggtcctgt attgccagat cgggaacaaa tgaatctgtg gatgcatcaa      240
gctatcgtea gtcaaacccc tttaaaatgt tgctttggct ttgtaaattt aaatatgtaa      300
gtgctatata agtcaggagc agctgtcttt ttaaaatgtc tcggctagct agaccacaga      360
tatcttctag acatattgaa cacatttaag atttgaggga tataagggaa aatgatatga      420
atgtgtattt ttactcaaaa taaaagtaac tgttacgttg cgaaaaaaan nnnnnnnnnn      480
naaaaaaaag tnccttgggc cgggaccacg ctagggcaaa tccagcacac tggcggccgt      540
actagggatc cactnggacc agctggcgna atatggnn

```

<210> 461
 <211> 425
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(425)
 <223> n = A,T,C or G

```

<400> 461
acgcgggggct ttctggtctc ggccgcagaa gcgagatgac gaagggaacg tcacgttttg      60
gaaagcgtcg caataaga ag cacacgttgt gccgcgcgtg tggctctaag gcctaccacc      120
ttcagaagtc gacctgtggc aaatgtggct accctgccaa gcgcaagaga aagtataact      180
ggagtgccaa ggctaaaaga cgaaatacca ccggaactgg tcgaatgagg cacctaaaaa      240
ttgtataccg cagattcagg catggattcc gtgaagggaac aacacctaaa cccaagaggg      300
cagctgttgc agcatccagt tcatcttaag aatgtcaacg attagtcatg caataaatgt      360
tctggtttta aaaaatnnan nnaannntn nttnaaanaa aaaaagtnct nggccngac      420
cacgc

```

<210> 462
 <211> 581
 <212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1) ... (581)

<223> n = A,T,C or G

<400> 462

```

ggtactattg acccagcgat gggggccttcg acatgggctt tagggagtc taagtggagt      60
ccgtaaagag gtatctttac tataaaagct atttgtgaag ctagtcatat taagttgttg      120
gctcaggagt ttgatagttc ttgggcagtg agagtgaagta gtagaatgtt tagtgagcct      180
aggggtgttg gagtgtaaat tagtgcgatg agtaggggaa gggagcctac taggggtgtag      240
aataggaagt atgtgcctgc gttcaggcgt tctggctggg tgcctcatcg ggtgatgata      300
gccaaagggt ggataagtggt ggtttcgaag aagatataaa atatgattag ttctgtggct      360
gtgaatgtta taattaagga gatttgtaag ggagattagt atanagaggt anagtttttt      420
tcgtgatagt ggntcactgg ataantggcc gttggctttg ccatgattgt gaggggtagg      480
agtcaagtag ttagtattan ganggggggtt nttaggggtc cnaggaaang ttggggaana      540
ctaaannggt gtnngtnattn gtaaaaaata nnnnanggat n                        581

```

<210> 463

<211> 574

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1) ... (574)

<223> n = A,T,C or G

<400> 463

```

actgtgtggc gccttattct aggcacttgt tgggcagaat gtcacacctg ccgatgaaac      60
tcttgcgtaa gaagatcgag aagcgggaacc tcaaattgag gcagcgggaac ctaaagtttc      120
agggggcctc aaatctgacc ctatcggaaa ctcaaaatgg agatgtatct gaagaaacaa      180
tggaagtagt aaagggttaa aaatcaaaac aaaagcccat gaatgtgggc ttatcagaaa      240
ctcaaaatgg aggcattgtc caagaagcag tgggaaatat aaaagttaca aagtctcccc      300
agaaatccac tgtattaagc aatggagaag cagcaatgca gtcttccaat tcagaaccaa      360
aaaaaaaaaa naaaaaaaag tacttttttt ttttnnnntt ttttttttt taggtaattg      420
gtgttgagct tgaacgcttc cttaattggn ggctgctttt angcctctat ggggtgttaa      480
ttttttactc tcttacaagg tttttcctaa gtccaaanac tgtccttttg gctacagtta      540
aatttccagg ggattaaagg gttttgggcn aatt                                574

```

<210> 464

<211> 580

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1) ... (580)

<223> n = A,T,C or G

<400> 464

```

ggtacctagt aagctctccc tctctccacc ctccaccctc aaggaggccc cagtgtcagt      60

```

tggtccccc	tc	tggggtccatg	agttctttatc	atttagctcc	cacttataag	caagaacatg	120
cagtatttg	g	ttttctgttc	ctgccttagt	ttgctaagga	taacggcctc	cagctccatc	180
cagttcctg	c	aaaggacatg	atcctgttct	ttctatggct	gtatagtatt	ccatgggtga	240
tatttaccac	a	attgtcttta	tccagtctgt	cattgatggg	cttttgggtt	gatttagtagc	300
tttttgaatg	t	gtaacttttc	tacagaagta	cgcggggctt	ttttttttgc	tgtaggcccg	360
ggtgggttgc	t	gccgaaatgg	gcangttcat	gaaacctggg	aagggtggtgc	ttgtcctgct	420
ggacgctact	c	ncggacgcaa	agctgtcatc	gtgaaagaac	attgatgatg	gcaccttana	480
cgcctacag	c	ccatgctctg	gtggctggaa	ttgaccgcta	cncgccgaaag	tgacagctgn	540
catgggcaag	a	aagaagatcg	ccagagatca	aagataaaan			580

<210> 465

<211> 578

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1) ... (578)

<223> n = A,T,C or G

<400> 465

ggtacttttt	t	tttttttttt	tttttttttt	ttctacatca	ctttanaata	tttattgtat	60
tccttaatgc	a	atttcttaac	atgtatagca	ctctttaatc	aagaatataa	agtcactctac	120
ttagaatcac	a	attatcttaa	agatgcatac	tggaatgata	agtttgaaga	tgtaactatc	180
aacaattctt	t	ttcaaaatca	tatcaatata	ttactctcat	ggaacttgca	cattctaaga	240
agggtcattt	t	ttcccccca	gtaccaatat	tacattatct	gacagggata	ataaaatgag	300
cagagactgg	a	aatcacaga	caataacatt	gctttctcaa	ttaacagaaa	ggattcataa	360
catattcctt	a	acggtagat	gtgatttgta	gagaatgtgg	aaaagaacta	ttgagaagtc	420
cacctgctgc	c	caaaactgag	gcacattagg	gtggttgtgg	gangagttat	atttgagggg	480
ccatttttcc	t	taggggttta	aaagcatgtc	cngggttgng	gtnatttgcc	attaagtctn	540
ttttcaata	a	aaagaattag	gggagaaaag	ttggaaaa			578

<210> 466

<211> 546

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1) ... (546)

<223> n = A,T,C or G

<400> 466

accaatacca	c	caattttgt	agacatcctg	gagaggcagg	cgcaagggct	tgctcagttgg	60
acgagttgg	t	ggtaggatgc	agtcacagag	ctcaagcagc	gtgggtccac	tggcattgcc	120
atccttacgg	g	tgactttcc	atcccttgaa	ccaaggcatg	ttagcacttg	gctccagcat	180
gttgtcacca	t	tccaaccag	aaattggcac	aaatgctact	gtgtcgggg	tgtagccaat	240
tttcttaatg	t	taagtgtga	cttcttaac	aatttctctc	tatctcttct	ggctgtaggg	300
tggtcagtg	g	aatccattt	tgtaaacacc	gacaattagt	tgtttcacac	ccagtgtgta	360
agccagaang	g	catgctctc	gggtctgccc	attcttggag	ataccagctt	caaattcacc	420
aacaccagca	g	caacaatca	ggacagnaca	gtcggnctga	gatgtccctg	taatcatgtt	480
ttgataaaag	t	ctctgtgtc	ctggggcatc	aatgatagtc	acatagtacc	tcggccgcga	540
ncacgc							546

<210> 467
 <211> 445
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(445)
 <223> n = A,T,C or G

<400> 467
 acctaaaacc cgaagaacct tctgtaagaa gtgtggcaag catcagcctc acaaagtgc 60
 acagtataag aagggcaagg attctttgta tgcccagga aggagcgct atgatcggaa 120
 gcagagtggc tatggtgggc agacaaagcc aattttccgg aagaaggcta agaccacaaa 180
 gaagattgtg ctaaggctgg aatgtgttga gcctaactgc agatccaaga ggatgctggc 240
 tattaagaga tgcaagcatt ttgaactggg aggagataag aagagaaagg gccaagtgat 300
 ccagttctaa actttgggat atttttcttc aattttgaag agaaaatggg gaaccataga 360
 aaagttaccc gagggaaaat aaatacagt atattccaaa aaaaaaann nnnnnaaaaa 420
 aaagtncttg gccgggaccc cctaa 445

<210> 468
 <211> 566
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(566)
 <223> n = A,T,C or G

<400> 468
 actgtgtggc gccttattct aggcacttgt tgggcagaat gtcacacctg ccgatgaaac 60
 tcttgcgtaa gaagatcgag aagcggaacc tcaaattgcg gcagcggaac ctaaagtttc 120
 agggggcctc aaatctgacc ctatcgaaa ctcaaaatgg agatgtatct gaagaaacaa 180
 tgggaagtag aaaggttaaa aaatcaaaac aaaagcccat gaatgtgggc ttatcagaaa 240
 ctcaaaatgg aggcattgtc caagaagcag tgggaaatat aaaagttaca aagtctcccc 300
 agaaatccac tgtattaagc aatggagaag cagcaatgca gtcttccaat tcagaaccaa 360
 aaaaaaaaaa nnaaaaaaag tacttttttt tntnnnnnnn ttttttttag gaatgggtgt 420
 tgaacttgac ctttcttaat gggggctggg tttaggctat atggngtaaa tttttctctt 480
 ttacaagggt tttcctagng ncaaaaactg tcctttggac taccgtaaat tacagggggt 540
 taaaggttnt ggggcaatta aanttn 566

<210> 469
 <211> 586
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(586)
 <223> n = A,T,C or G

```

<400> 469
acgcgggata ggtttggtcc tagcctttct attagctctt agtaagatta cacatgcaag      60
catccccgtt ccagtgagtc caccctctaa atcaccacga tcaaaaggga caagcatcaa      120
gcacgcagca atgcagctca aaacgcttag cctagccaca ccccccacggg aaacagcagt      180
gattaacctt tagcaataaa cgaaagttaa actaagctat actaacccca ggggttggtca      240
atttcgtgcc agccaccgcg gtcacacgat taacccaagt caatagaagc cggcgtaaag      300
agtgttttag atcacccctt ccccaataaa gctaaaactc acctgagttg taaaaaactc      360
cagttgacac aaaatagact acgaaagtgg cttaacata tctgaacaca caatagctaa      420
gacccaaact gggattagat accccactat gcttagccct aaacctnaca gttaaatcaa      480
caaaactgct cgccagacac tgcagccaca gcttaaaaact caaggacctg cgggcttcat      540
atccctctag angacctgtc tgtaatcgat aaccccgatc aacctn                      586

```

<210> 470

<211> 487

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(487)

<223> n = A,T,C or G

```

<400> 470
acggccaggg ctattggttg aatgagtagg ctgatggttt cgataataac tagtatgggg      60
ataaggggtg taggtgtgcc ttgtggtaag aagtgggcta gggcattttt aatcttagag      120
cgaaagccta taatcactgc gcccgctcat aaggggatgg ccatggctag gtttatagat      180
agttgggtgg ttggtgtaaa tgagtgaggc aggagtccga ggaggttagt tgtggcaata      240
aaaatgatta aggatactag tataagagat cagggttcgtc ctttagtggt gtgtatgggt      300
atcatttggt ttgaggttag ttgattagat cattgttggg tggtgattaa tcngttgntg      360
atgaaatatt tggaggtggg gatcaatana gggggaaata gaatgatcag tacctcgccc      420
gcgaccacgc taagggccaa tccacacact ggcggncgta ctaatggatc ccaactcgga      480
ccagctt                      487

```

<210> 471

<211> 488

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(488)

<223> n = A,T,C or G

```

<400> 471
actgcggcgg gtaggcctag gattgtgggg gcaatgaatg aagcgaacag attttcggtc      60
attttgggtc tcagggtttg ttataatttt ttatttttat gggcttttgt gagggaggta      120
ggtggtagtt tgtgtttaat attttttagt ggggtgatgag gaatagtgtg aggagtatgg      180
gggtaattat ggtgggccat acggtagtag ttagttaggg cattcccgcg tacctatttg      240
tatttttggt agagacaggg ttttgccatg ttggccagga tggctctgaa ctactgacct      300
cagggtgatcc tcacgccttt atctcccaaa gtgctgcgat tacaggcatg aggcaccact      360
cctggccaca ttcttatatt taaaaaaaaa gcacaactct attgtctact ggtgttcttt      420
tacctgaagt tcaaaactcta gctcttcaaa aaaaaaaaaa aaaaaaagta cctnggccgc      480
naccacnc                      488

```

<210> 472
 <211> 586
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(586)
 <223> n = A,T,C or G

<400> 472
 ggtacttgat gccctccaag caattaaaac caagggcaaa cgagcccat tcacaaattt 60
 tgaccctct actctccttc cttcatccct ggatttctgg acctaccctg gctctctgac 120
 tcactcctct ctttatgaga gtgtaacttg gatcatctgt aaggagagca tcagtgtcag 180
 ctcagagcag ctggcacaaat tcagcagcct tctatcaaat gttgaagggtg ataacgctgt 240
 ccccatgcag cacaacaacc gcccaaccca acctctgaag ggcagaacag tgagagcttc 300
 attttgatga ttctgagaag aaacttgctc ttctcaaga acacagccct gcttctgaca 360
 taatccagta aaataataat ttttaagaaa taaatttatt tcaatattag caaagacagc 420
 atgccttcaa atcaatctgt aaaactaaga aacttaaatt ttagttctta ctgcttaatc 480
 aaataataat tagtaagcta gcaaatagta atctgtaagc ataagcttat gcttaaatca 540
 gtttagtttg aggaatcttt aaaattacca ctaantgatt gnatgg 586

<210> 473
 <211> 575
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(575)
 <223> n = A,T,C or G

<400> 473
 ggtacaaagg ggaaagggtg catgccaaact atcgaattat aggatatgta aaaaatataa 60
 gtcaagaaaa tgccccaggg cccgcacaca acggtcgcaga gacaatatac cccaatggaa 120
 ccttgctgat ccagaacgtc acccacaatg acgcaggaat ctatacccta cacgttataa 180
 aagaaaatct tgtgaatgaa gaagtaacca gacaattcta cgtattctcg gagccacca 240
 agccctccat caccagcaac aacttcaatc cgggtggagaa caaagatatt gtggtttttaa 300
 cctgtcaacc tgagactcag aacacaacct acctgtggtg ggtaaacaat cagagccacc 360
 tggtcagtcc caggctgctg ctctccactg acaacaggac cctcgttcta ctacgcca 420
 aagaatgaca taggacccta tgaatgtgaa atacagaacc cagtgggtgc caccgcant 480
 gcccantcac cctgaatgtc cgtatgagtc aatcctgccg gcggccgttc naanggcgaa 540
 ttccacacac tggcggccgt ctaatggatc cactc 575

<210> 474
 <211> 515
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(515)

<223> n = A,T,C or G

<400> 474

ggtacgtggg	ggactcaact	gaaatcatgg	cgtttgacag	cacttggaag	gtagaccgga	60
gtgaaaacta	tgacaagtgc	atggaaaaaa	tgggtgttaa	tatagtgaag	aggaagcttg	120
cagctcatga	caatttgaag	ctgacaatta	cacaagaagg	aaataaattc	acagtcaaag	180
aatcaagcgc	ttttcgaaac	attgaagttg	tttttgaact	tggtgtcacc	tttaattaca	240
acctagcaga	cggaactgaa	ctcaggggga	cctggagcct	tgagggaagt	aaacttattg	300
gaaaattcaa	acggacagac	aatggaaacg	aactgaatac	tgtccgagaa	attataggtg	360
atgaactagt	ccagacttat	gtgtatgaag	gagtagaagc	caaaaggatc	tttaaaaagg	420
attgaccatt	attcttggcg	cacagtccaa	aatncaaat	ggccagaaga	tctatattgn	480
acctgcccgg	gcggccgttc	gaaaggccaa	ttcca			515

<210> 475

<211> 580

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(580)

<223> n = A,T,C or G

<400> 475

acaaagatct	gacatgtcac	ccagggaccc	atttcaccca	ctgctctgtt	tggccgccag	60
tcttttgtct	ctctcttcag	caatgggtgag	gcggataccc	tttcctcggg	gaagagaaat	120
ccatggtttg	ttgccttg	caataacaaa	aatggtggaa	agtcgagtgg	caaagctgtt	180
gccattggca	tctttcacgt	gaaccacgtc	aaaagatcca	gggtgcctct	ctctgttggg	240
gatcacacca	attcttccca	ggttagcacc	tccagtcacc	atacacaggt	taccagtgtc	300
gaacttgatg	aaatcagtaa	tcttgccagt	ctctaaatca	atctgaatgg	tatcattcac	360
cttgatgagg	ggatcggggt	agcggatggg	gcgggcatca	tgagtcacca	gatgagggat	420
tcttttgtg	ccccaaagat	ctttctnact	ttgacaactt	gaccttggn	gcgaccacc	480
taaggcgaat	tcaccactg	gcggccgtct	aatggatccn	netcggncca	acctggnat	540
atggcntaan	tnntccnggn	naaatntntc	ccncaatcc			580

<210> 476

<211> 593

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(593)

<223> n = A,T,C or G

<400> 476

ggtactatgt	gggacagtat	tttgcaaata	caagaagagc	tcagggcagc	tgtggagctg	60
gatggtctgc	ctggcaggcc	tctgtgcagt	ctgcctgtc	atcctgtccc	ctttttgggg	120
cttgatcctc	ttctcgggtg	catgcttctc	catgtatact	tacttatctg	gccaagaatt	180
gttacctgtg	gatcagaagg	cagtcctggg	gacaggtgtg	attgcgggct	tggccatgct	240
ttgtgcaagt	atctggatga	gctgggcttc	acggtatttg	ccggagtttt	gaatgaaaat	300
ggcccaggag	ctgaggaatt	gcgaagaacc	tgctctccgc	gcctctcggt	gctccaaatg	360
gacatcacga	accagtgcag	ataaaaagatg	cttacagcaa	ggttgcaaca	atgctgcagg	420

```

acaaaagact gtgggctgtg atcaacaatg ctnggggtgct tggccttttcc actgatgggg 480
agcttnttnt tatgatgact acnaacaatc ntqcccgnga acttttttga actgngaggg 540
acaaaacgtt tttccttttt taaaaaancc auggngnggtg gnnaattncn nnt 593

```

```

<210> 477
<211> 595
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1) ... (595)
<223> n = A,T,C or G

```

```

<400> 477
actacaagggt ttagcatttg ctctgctggt cgacattccc ccagtctatg ggttggtatgc 60
atcctttttt ccagccataa tctacctttt ctctcgccact tccagacaca tatccgtggg 120
tccgtttccg attctgagta tgatgggtggg actagcagtt tcaggagcag tttcaaaagc 180
agtcccagat cgcaatgcaa ctactttggg attgcctaac aactcgaata attcttcact 240
actggatgac gagaggggtga ggggtggcggc ggccggcatca gtcacagtgc tttctggaat 300
catccagttg gctttttggga ttctgcggat tggatttgta gtgatatacc tgtctgagtc 360
cctcatcagt ggcttcaacta ctgctgctgc tgttcatggt tttggnttcc caactcaaat 420
tcatttttca agtgacagtc ccgtcacaca ctgatncagt ttnaatttta aaagtacctc 480
ggccgcganc accctaaggc gaatttnaac ccactngcgg ccgttctant ggatccaact 540
ngnnncaaac ttngngaata ngggcataac ngntcctggg gaaatnnttc ccnct 595

```

```

<210> 478
<211> 420
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1) ... (420)
<223> n = A,T,C or G

```

```

<400> 478
ggtacacagt atgtataaca atgcatacta tgggtgtggag ttaattccaa ttaccatatt 60
ttatatattat tggtcacaac agcatacatt ttatgctcca aaatacatgg atctgacaaa 120
atggttacat ttaatgttct tttaaagaaa gatgaactaa atttaagaag aattggtttt 180
tcctaataatc tcattttcaa attactgata caaatttgcc agagaaacaa ttacatgttt 240
tacctaacat caaataatct ccagtttcta agacagatgc atttcttggt caatttccaa 300
aagtaataaa aggcctttcta actgaaaaca tttgcatccc tagctctcta aagtaattaa 360
aaagaaaatt acaaaaaatg acctctaagc ttctgaacag ccacttant tacataaagt 420

```

```

<210> 479
<211> 602
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1) ... (602)

```

<223> n = A,T,C or G

<400> 479

ggtacctagt	cagatggtag	acgagctgtc	tgctgcccga	ggagcacctc	tatacaggac	60
ttagaagtag	tatgttattc	ctgggttaagc	aggcattgct	ttgccctgga	gcagctatct	120
taagccatct	cagattctgt	ctaaaggggt	tttttgggaa	gacgttttct	ttatcgccct	180
gagaagatct	accccaggga	gaatctgaga	catcttgccct	acttttcttt	attagctttc	240
tcctcatcca	tttcttttat	acctttcctt	tttggggagt	tgttatgcca	tgatttttgg	300
tatttatgta	aaaggattat	tactaattct	atttctctat	gtttattcta	gttaaggaaa	360
tgttgagggc	aagccaccaa	attacctang	ctgagggttag	agagattggc	cagcaaaaac	420
tgtgggaaga	tgaactttgt	cattatgatt	tcattatcac	atgattatag	aaggctgtct	480
taatgcaaaa	aacatactta	catttnanac	atattccaan	gggatctcnc	attttgtaaa	540
aagttgacta	ttactggagt	aaacctgtt	ttcccttant	ttaacttttt	ttgggaaatt	600
at						602

<210> 480

<211> 600

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(600)

<223> n = A,T,C or G

<400> 480

ggtacttttt	tttttttttt	tttttttttc	ggtttgaggg	ggaatgctgg	anattgtaat	60
gggtatggan	acatgtcata	taagtaatgc	tagggtagt	ggtaggaagt	tttttcatag	120
gaggtgtatg	agttggctgt	agcggaatcg	ggggtatgct	gttcgaattc	ataaaaacag	180
ggaggttana	agtagggctt	tggtgacaaa	atatgttggt	taaagttcag	ggganagtgc	240
gtcatatggt	gttccttagga	aaattgtagt	ggtgaggggt	tttattataa	taatgtttgt	300
gtattcggct	atgaaaaata	gggcgaaggg	gcctgcggcg	tattccatgt	tgaagcctga	360
gactagttcg	gactccccct	cggcaaggtc	caaaggggtt	ccggttggtc	tcttctagt	420
tggagataaa	tcatattatg	gcnaggggtc	atgatggcag	gagtaatcaa	aggggtcntt	480
tgttttgaaa	aagggnggan	aggttaaagg	ancccccttt	tataatgggt	atantaaaaa	540
gatgcttggg	ggactcnttt	aaaatgttgg	ctcttcttcc	angcnccac	aggcgatatt	600

<210> 481

<211> 594

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(594)

<223> n = A,T,C or G

<400> 481

cgaggtacgg	ccagggctat	tggttgaatg	agtaggctga	tggtttcgat	aataactagt	60
atggggataa	gggtgttagg	tgtgccttgt	ggtaagaagt	gggctagggc	atttttaatc	120
ttagagcgaa	agcctataat	cactgcgccc	gctcataagg	ggatggccat	ggctagggtt	180
atagatagtt	gggtggttgg	tgtaaattag	tgaggcagga	gtccgaggag	gttagttgtg	240
gcaataaaaa	tgattaagga	tactagtata	agagatcagg	ttcgtccttt	agtgttngnt	300

atggttatca	tttgttttga	ggttagtttg	attagtcatt	gttgggtggt	gattantccg	360
ttgttgatga	gatatttgga	ggtgggggac	aatagagggg	gaaatagaat	gatcagtacc	420
tgcccnngcg	gncgctcgaa	anggcgaatt	ccaccacact	ggcgggcnnt	ctaattggatn	480
cgaccnngtc	ccaacttgcg	taatcatggc	atacttgtn	ctggtgaaat	ggtatccctc	540
acaattccca	cacatacaac	ccgaacctaa	atgtaaanct	gggggcctat	natn	594

<210> 482

<211> 600

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1) ... (600)

<223> n = A,T,C or G

<400> 482

accatgaaat	acatatat	cataaggttc	agttacaaaa	tggattgttt	caaattggcaa	60
tttcttacac	taacctgatt	atgaaaaaaaa	gaagtctgta	tcattctgctt	ccaagtctgt	120
tatgtccaaa	tatattttaa	ttatgcattt	attttgtac	ttttataaat	attagagatt	180
tcaccttaaa	ttatttttgt	aactagttct	agaacatggt	ttccaattat	tatttttcta	240
atggagacat	ataattgacc	tatgtttatg	catatatgtt	ctctacacag	tgaaactttt	300
tttaaaaaaga	atagtaaaga	aaatgcggaa	gctctggctc	tccaaggcaa	agtcaaaaaa	360
aaaaaaaaaag	cgggggggaa	tgcgagggaac	attttattac	acctnctgat	tttctcctt	420
gagntttatt	ttctccctt	ggntatttgt	taatgctaga	aactgnattc	ctaanaaagc	480
atacctcttt	cagngagcn	tgataattgg	gaanaatttt	gttcctttag	tntgaacatt	540
ttattaagaa	gngattccta	ataaaganac	aangggctnt	ttaattnttt	gggggnngga	600

<210> 483

<211> 605

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1) ... (605)

<223> n = A,T,C or G

<400> 483

acagaacatc	gtcagcacta	gcacagttta	cagaacctca	cagacccaaa	ggaacatcaa	60
taggcaaagc	gactacagga	ggcgtgtgtc	cgcgtgggcg	aggtaaagag	ggtcagtatt	120
ggtcaagtga	cagtgtcggt	aatctggcaa	gacagtgatg	ttaagaagggt	tcatagttta	180
agaattatct	aaaatatttt	aaaaactata	aagctgcaac	acatgatttt	tacacctagt	240
tactagaaaa	ctaaggaaaag	cacttattag	ctctgaataa	agtaacatgg	aaagcaccct	300
tactaatcga	caaaaaaac	ttctaattgca	ttatcagaaa	gattttataa	tacaaggagg	360
catattgctc	agtcagaagg	ggttctataa	gaaaagcact	tactaagtta	gcgactaaca	420
gaacaaccng	tttaagatg	aattaaatgc	cccatttggg	gangcatggc	aggtgttaag	480
anaaangaaa	agcntaagaa	aacatttntc	ggttatanca	aaccttntt	tnttatctac	540
tgnatttgac	aaaaattaac	cntttaaagt	tttaccnngg	cacttnnttc	nttgcctcgc	600
gcccg						605

<210> 484

<211> 591

<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(591)
<223> n = A,T,C or G

<400> 484
 ggtacgcggg tggggagacc ctggggtagc agccactgac ctcacacctg gaggaagctg 60
 tgtgaccgat tcatgagctt atgcctgaag acagagcaag cactccccgc accacgacga 120
 tgacgttcac ttgttttgtg tttttcgatc tcttcaacgc cttgacctgc cgctctcaga 180
 ccaagctgat atttgagatc ggcttttctca ggaaccacat gttcctctac tccgtcctgg 240
 ggtccatcct ggggcagctg gcggtcattt acatcccccc gctgcagagg gtcttccaga 300
 cggagaacct gggagcgctt gatttgcgtt ttttaactgg attggcctca tccgtcttca 360
 ttttgtcaga gctcctcaaa ctatgtgaaa aatactgttg cagccccaaa gagagtccag 420
 atgcaccctg aaagatgtgt agtggaccgc acttccgcgg naccttctta atnatttcaa 480
 ctgggtgnga ctgtggcctt gccctgtttc ttcttagggg agactttang anggcgagcn 540
 tcataccgga tagttttctt taggaaactn aggaaccttg gctcaggacc a 591

<210> 485
<211> 605
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(605)
<223> n = A,T,C or G

<400> 485
 ggtacgcggg gatataaagg gagagagcaa gcagcgagtc ttgaagctct gttnggtgct 60
 tnggatccat ttccatcggn ccttacagcc gctcgtcaga ctccancagc caanatgggtg 120
 aancagatcg agagcaagac tgcttttcan gaagccttgg acgctgcang tgataaactt 180
 gtagnagttg acttctc j c cacgtgggtg gggccttgca aaatgatcaa gcctttcttt 240
 cattccctct ctgaaaagta ttccaacgtg atattccttg aagtagatgt ggatgactgt 300
 caggatgttg cttcagagtg tgaagtcaaa tgcattgccaa cattccagtt ttttaagaag 360
 ggacaaaagg tgggtgaatt ttctggagcc aataaggaaa agctttgnag ccnccattaa 420
 tgaatgagtc taatcatgtt ttctgaaaac ataaccagc catttggtta tttaaaactt 480
 gnaanttttt nagntaccna aattttaaagt ctgaagacat aaccgcgtgc catttgcggtg 540
 acaatnaaaa attatgccaa cacttttttna anaanganan nnntttcctn gggaaatngt 600
 anccc 605

<210> 486
<211> 319
<212> DNA
<213> Homo sapiens

<400> 486
 ggtaccagtt gttagcataa agattctggg actcattatg gactactaga aggacctcct 60
 tcccttctgc gacattgaac ggcacgacat caatattggt ctgggcactg tttggcaggt 120
 tccagaaggt taaaagcgag gctgtgagca ggagtccttg ccagggaatg cacactctgt 180
 atggacaggc tgaaggggac cccatggtct ctgctgcctg cttgtcctct gtggagaaga 240

gcttgggctc caggaactct cttgtcaggg ctgctgtgac tgtcagctct gctgtccttc 300
ctacctctgt gtcccgcgt 319

<210> 487
<211> 586
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(586)
<223> n = A,T,C or G

<400> 487
acgcgggagc tgagtgtccc gcggggcccg aagcgtttac tttgaaaaaa ttagagtgtt 60
caaagcaggc ccgagccgcc tggataccgc agctaggaat aatggaatag gaccgcgggt 120
ctattttgtt ggttttcgga actgaggcca tgattaagag ggacggccgg gggcattcgt 180
attgcgccgc tagaggttaa attcttggac cggcgcaaga cggaccanag cgaaagcatt 240
tgccaagaat gttttcatta atcaagaacg aaagtcggag gttcgaagac gatcagatac 300
cgtcgtagtt ccgaccataa acgatgccga ccggcgatgc ggccggcgta ttccatgacc 360
cgccgggcag ctttcnggaa accaaagtct ttgggttncg gggggagtat ngttcnaaaa 420
aaaaaaaaaa aaaaaaaagt cctnggcccg gancccttta ngngaaatt cagccactgg 480
nggcgttctn atggatncna gctcggncca acntggcgta atatggcata cttgttctcg 540
gngnaaatgt ttccctccaa attccccaaa tacgggcgga gcttaa 586

<210> 488
<211> 487
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(487)
<223> n = A,T,C or G

<400> 488
acagctgggt ggacctattc atgcatcttc accagcagct ggagcatctc cacccttgggt 60
atctctgggt taaattactt gagctctgtg ctttgaaacc agtttgataa gtcctttact 120
aaggagctcc tgaagggtcg ccttgccag ggagcctcga atcttcagtc tctcagagac 180
cacagctggg gttataagtt tatagttggg aacttcctta cagagtttat cataggtagc 240
tttgtcaaac aagactaagt tattgagctt gtcccgaact ttgcctttgg accacttctt 300
ctttttggcc ttgcccccg atttggtcac tgggtctttg tctttcttgg ccgaacttcc 360
agcgtccttc ttcttcttgt cgtccttaag cggccttgcg aanctcggag aataagcaac 420
aaacaccgca cctcgtcnaa gatgtcggac aaaaaaaggc cccgcgtacc ttnggccgcg 480
ancacnc 487

<210> 489
<211> 589
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature

<222> (1)...(589)

<223> n = A,T,C or G

<400> 489

```

acgcgggggtc tctcctcagg cagcagcaac gcggaggaaa cgggagtgaa cggagagcgt      60
agtgaccatc atgagcctcc tcaacaagcc caagagttag atgaccccag aggagctgca      120
gaagcgagag gaggaggaat ttaacaccgg tccactctct gtgctcacac agtcagtcaa      180
gaacaatacc caagtgtcga tcaactgccg caacaataag aaactcctgg gccgcgtgaa      240
ggccttcgat aggcactgca acatggtgct ggagaacgtg aaggagatgt ggactgaggt      300
acaaagatta aattaagaca cggtaaattg actaaatatt tggtttttat ataaataaag      360
gtcataacca caccgttgac atgtaatact gttataatac aacagttaaa ctttgtgagt      420
ctcaacagaa gtcactctga gttnaacagg aaacaaaagt tgaaaaaaaa catgttnaaa      480
caaaactctg ggactaacag gtcgggattg taagtacaac caacatattc ctcacttctg      540
ggtntttcaa gtttacagta cttggccgga cccctttang ggnattcac      589

```

<210> 490

<211> 591

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(591)

<223> n = A,T,C or G

<400> 490

```

ggtaccggga tagtttttgc agggttttat tttataaaat ccaagcgcgc tgttgattgt      60
gttttccttg ttttcagccc cccgactcca gccgcagca catttccgct gtccgctcagt      120
aattgtgtcc tctcttttat cttgcttggg gaatgttgtt ttctgactag gctgatcatt      180
atctaagaaa tctaattctg ttgattttta aaacttttag gaccataaac gttgtgttca      240
tatatggaca tggaaatatt tatataattt tatagaaaat aaccttttag atggtcaaag      300
tgtaaggagt tttttttgtc agataatcat ttctacttca aaaacatttc atgcaatatt      360
agaataaagt tcctgtcatt cctctnnnan aaaaaannnn nnnnnnnanna nnnnnnnnnn      420
nggaanannn nnnnnnnnnn aaaaaagtac ctgccnnggc ggccgttcaa aaggcgaatt      480
ccaccactg gcggccgttc taatggatcc anctcggacc aacctggnga aacatggcat      540
acctgttctt gngnaaatgg tntcccttac aattcccaca aataaaaccg g      591

```

<210> 491

<211> 583

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(583)

<223> n = A,T,C or G

<400> 491

```

ggtacatata aatccttttg gtgtcacttg tagcaagcct tgcttctgca gttttcggat      60
tttcctcaaa gctttgttgc gcttgcgtag aattcgaagt ggactaaagc caacagcatc      120
gataagtttc cgctaaaga aaccaatggt tgcaaagtag ataggagatg gacatctgaa      180
aattttcact ccttctggct catacatatc ataataatct tttttattct tatagatggt      240
ggttcttcca atattagcca gcgtgctgca ttttggaat tgggtcctga acacgatggt      300

```

tagcagttga	aatgccacac	tagctgccag	gcctaaccgc	agtcccagga	caatgggtgaa	360
agatgaaaagg	catgaaccca	aataaacaat	catatttggn	cnttccccca	atctgctatt	420
ttaaccaact	gcatcaacat	tcctttaagt	tccaatgcta	aactggcang	acnggcnttt	480
gtagaagngc	cangaaaaat	cagncttga	cgacaatcac	accatgatgn	nccataancc	540
acaatctggg	nttggtcnn	ggcctctgaa	cnnngactgg	nag		583

<210> 492
 <211> 597
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(597)
 <223> n = A,T,C or G

<400> 492	
acgcggggggg	tggcacggag gaaccaggag cgtgccctgc gcaccgtctg gagctccgga 60
gatgacaagg	agcagctggt gaagaacaca tatgtcctgt gaccgccctg tcgccaagag 120
gactgggggaa	gggaggggag actatgtgtg agcttttttt aaatagaggg attgactcgg 180
atttgagtga	tcattagggc tgaggtctgt ttctctggga ggtaggacgg ctgcttctctg 240
gtctggcang	gatgggtttg ctttggaat cctctangag gctcctctct gcattggcctg 300
cagnctggca	acaaccccg gttgtttcct cgctgatcga tttctttcct ncaggtagag 360
ttttctttgc	ttatgttgaa ttccattgcc tttttctcat cacaaaaaat gatgttggga 420
atcgnntcct	ttgtttggct gaattatggg ntnttttaant ataaaccaa nttttttatt 480
aacattctta	aanaaggga agtnnaatgt ncnttggnc cnaaccncgt aanggcnaat 540
ttcancctt	ggnggccgtn ntnnggatc cnnncnngnn ccaannntgg nntantn 597

<210> 493
 <211> 591
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(591)
 <223> n = A,T,C or G

<400> 493	
acggatgcta	cttgtccaat gatggtaaaa gggtagctta ctggttgctc tccgattcag 60
gttagaatga	ggaggtctgc ggctaggagt caataaagtg attggcttag tgggcgaaat 120
attatgcttt	gttgtttgga tatatggagg atggggatta ttgctaggat gaggatggat 180
agtaataggg	caaggacgcc tcctagtgtg ttaggggacgg atcggagaat tgtgtaggcg 240
aataggaaat	atcattccgg cttgatgtgg ggaggggtgt ttaaggggtt ggctagggtgta 300
taattgtctg	ggtcgcctag gaggtctggt gayaatagt ttaatgtcat taaggagaga 360
aggaagagaa	gtaagccgag ggcgtctttg attgtgtagt aagggtggaa ggtgatttta 420
tcggaatggg	aggtgattcc taaggggggt gttgatcccc tttcctgccca agaataagaa 480
gtggaatgct	gctagggtg cattaatgaa ggccaagatg aaatgaaagg taaanaatcn 540
ngtgangggg	gactgctact gatanccctc caaatcatga ataggntgtc c 591

<210> 494
 <211> 374
 <212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(374)

<223> n = A,T,C or G

<400> 494

ggtacttttt	tttttttttt	tttttttttt	tttttttagnt	catgtctttt	attaactcat	60
acagttactt	gtcttctggt	ttgttgaaac	agtaagtcan	acaacatttg	ccacaataat	120
gtctgtcaaa	gtgacttgcc	ataaacaccc	cagcaccaca	ttcatcanaa	gggcactctc	180
gacgaaggcg	actaattttg	ccattctcat	ccaccttata	atatttcagg	acagccagct	240
taaccttctt	tctcttggtc	ttattcttct	tgggagnggt	gtaagacttc	ttcttctttt	300
tcttagcacc	accacgaagt	ctcaacacaa	gatgaagagt	agactccttt	tgaatattgt	360
aagtcagaca	aagt					374

<210> 495

<211> 597

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(597)

<223> n = A,T,C or G

<400> 495

actgggagaa	ggtgctgacg	ccgacgaagt	ggtggatggg	cttcccgtg	caggtgaacc	60
tcttggtgcc	atcctgcagg	gtcccccgag	gattgcctag	atcatttttc	aagcagtagt	120
tgctttctgg	gtttttacaa	attctgcatt	ttccacactg	aggagtaaag	agcgggatga	180
ctttatcacc	tggtttgact	gtagtcaccc	cttctccaac	actttccacg	atgccggctg	240
cctcatggcc	taaaatcaca	ggaagggggg	tcaccagggt	gccactaacc	acatgctcat	300
ctgaacgaca	gattcctgca	gccaccatct	taatgcgaac	ttcatgagcc	ttaggaggtg	360
caacctctac	ctcctcaatg	gaaaagggtt	tctttaactc	ccatagcaca	actgctttgc	420
atttgattac	ctgtaaactc	agctacttgt	gaaggctgag	gcanganaat	actttgaacc	480
ccggaaggca	aaggttgcaa	tgagccnana	acaccattgn	acttccanct	gggcaatana	540
aaaaaactca	tttttctctg	tggtcacaat	gatctgcttc	ttgcaaacaa	gagntgn	597

<210> 496

<211> 604

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(604)

<223> n = A,T,C or G

<400> 496

ggacgcgggt	gctgactgca	tagctctttt	tcttgagagg	ctctccattt	tgattcagaa	60
agtttagcata	tttattacca	atgaatttga	aaccagggct	tttttttttt	tttgggtgat	120
gtaaaaccaa	ctccctgcc	ccaaaataat	taaaatagtc	acatttatct	ttattaggta	180
atcacttctt	aattatatgt	tcatactcta	agtatcaaaa	tcttccaatt	atcatgctca	240

```

cctgaaagag gtatgctctc ttaggaatac agtttctagc attaaacaaa taaacaaggg      300
gagaaaataa aactcaagga gtgaaaatca ggaggtgtaa taaaatgttc ctgcgattcc      360
ccccgcgttt tttttttttt ttgacttttg cttgggaaagc cagagcttcc cgcattttct      420
ttactattct ttttaaaaaa agtttctact ngtaaaagaa catatttgcc taaacatang      480
tcaattatat gtctccatta naaaaaaata attggnaaac attgtctana actagttcca      540
aaataattaa ggggggaaatc tntaatnttt ttaaagtgcc naaanaatgc ctaanttaaa      600
antt                                              604

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<210> 497
<211> 587
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(587)
<223> n = A,T,C or G

```

```

<400> 497
acattaatga aatgtttcca aagaaatact gaacaatata tactctagtt tgctgaggtt      60
ccagctcgag ttcaaacctt attcttgtgc aataaaaatc agcatggatc ttagatgatc      120
tagaatacac tgtgttttga aatccacagc tgggttctatt ttaaccatt atgaaaaacc      180
agtacttttt tttttttttt tttttttttt nctnggacca taaattttta ttggcaggtc      240
aggaaaaaag ccggggggtaa ggggtcccttc ctcccatccc ctctacccan aanacaccct      300
ccaaaggaca gcagaagccc cagagcctgc tgccctcagag gaccttggag gcagacaaat      360
tgttgtagn g atcttcctgt cctcaanca ggctgcggta ggtggnaatc tinctgtcca      420
gccgcgactt gatgtccatg aaccgctggt cctcgccgcg gacaccctta nggcgaattn      480
caccnactgg gnggcgttct agtggatccg actcggacca acctngcgna atcatggcan      540
actggttinct gnnggaaatg gtttccctnc aattccccaa cataccn                      587

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<210> 498
<211> 354
<212> DNA
<213> Homo sapiens

```

```

<400> 498
acgcggggcaa taaagctaaa actcacctga gttgtaaaaa actccagttg acacaaaata      60
gactacgaaa gtggctttta catatctgaa cacacaatag ctaagaccca aactgggatt      120
agatacccca ctatgcttag cctaaaacct caacagttaa atcaacaaaa ctgctcgcca      180
gaacactacg agccacagct taaaactcaa aggacctggc ggtgcttcat atccctctag      240
aggagcctgt tctgtaatcg ataaaccccg atcaacctca ccacctcttg ctgagcctat      300
ataccgccat cttcagcaaa cctgatgaa ggctacaaag taagcgcaag tacc                      354

```

```

<210> 499
<211> 632
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(632)
<223> n = A,T,C or G

```

<400> 499

nccgaggtac	caactgcact	cgttttggca	ttgcagctaa	atatcagttg	gatcccaactg	60
cttccatttc	tgcaaaagtc	aacaactcta	gcttaattgg	agtaggctat	actcagactc	120
tgaggcctgg	tgtgaagctt	acactctctg	ctctggtaga	tggaagagc	attaatgctg	180
gaggccacaa	ggntgggctc	gccctggagt	tggaggctta	atccanctga	aaagaaacct	240
ttgggaatgg	atatcaaaag	aattggcctt	aatatatttc	cattgngacc	agcagcaggc	300
tttttttccc	ccagaagatg	atcaaaacaa	aaggatgatc	tcaacaagaa	ctgtatttta	360
aagtatttaa	ganagtcttt	ggtaactnng	ttctaagtng	gtatctaatt	acccaatgct	420
gcagtcttgc	agtccttatt	cattanttaa	atgtatttaa	ctggtaaatt	ccctnccnc	480
cataatgaaa	taganccttt	ttgaaaaccc	aaaaaaaaaa	aaaaaaaaaa	aaaaaagtcc	540
ctgcccgggc	ggccctcaaa	ngngaattc	cannccctgg	gggccgtact	aanggatccn	600
cccgnccaa	cttggggaat	atgggntant	gn			632

<210> 500

<211> 619

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(619)

<223> n = A,T,C or G

<400> 500

tccagcggnc	cgccgggcn	gtcatctata	aaaggaaaag	tgatggcatc	tatatcataa	60
atctcaagan	gacctgggag	aagcttctgc	tggcagctcg	tgcaattgtt	gccattgaaa	120
accctgctga	tgtcagtgtt	atatcctcca	ngaatactgg	ccaaaaggct	gtgctgaant	180
ttgctgctgc	actggaacca	ctccaattgc	tggccgcttc	actcctggaa	ccttcactaa	240
ccagatcagg	caaccttccg	ggaccacggn	ttnttgtggt	tactgacccc	aaggctgacc	300
accaacctnt	cacggaggca	ttttatgtta	acctacctac	cattgctgctg	tgtaacacaa	360
gattcttctc	tgcctatgtg	gacattggca	ttccatgcaa	caaccaaggg	gagctcactc	420
aatgggtttg	atgtggtgga	tctgctcggg	naagtctgcg	catgcctggc	accatttccg	480
tgaacaccat	ggagggatgc	ctgattttac	cttggccgga	cacnctangg	cgaattcacc	540
acttggngcc	gtatantgga	tccactcgga	ccaacttggg	naaaatggca	naatnttccg	600
gggaaatgat	ccctccaan					619

<210> 501

<211> 605

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(605)

<223> n = A,T,C or G

<400> 501

accacactga	gatagtgttt	gccaggacct	cccctcagca	gaagctcatc	atttgtggaag	60
gctgccaag	acaggttgct	atcgtggctg	tgactgggtga	cggtgtgaat	gactctccag	120
ctttgaagaa	agcaaacatt	ggggttgcta	tggggattgc	tggtcagat	gtgtccaagc	180
aagctgctga	catgattctt	ctggatgaca	actttgcctc	aattgtgact	ggagtagagg	240
aaggtcgtct	gatctttgat	aacttgaaaa	aatccattgc	ttatacctta	accagtaaca	300
ttccccgaga	tcaccccggt	cctgatattt	attattgcaa	acattccact	accactgggg	360

actgtcacca	tcctctgcat	tgacttgggc	actgacatgg	gtnctgccat	ctcctggcctt	420
atgagcaggc	tggagggcat	catgaanaaa	cagcccaaaa	tccaaacaga	caacttgtga	480
atgancnggt	gacacatgg	ctatggcaga	atggatgac	nagnctggg	aggttcttac	540
ttacttggaa	tctgntgaaa	cggttcttcc	aatacctntt	ggcctccatg	gntggaanac	600
cctga						605

<210> 502
 <211> 627
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(627)
 <223> n = A,T,C or G

<400> 502						
acatcttgct	ggaaaatgct	gccagggct	ctggagacgg	tggctgcccg	ggctcccttc	60
actgtccagg	tcctgaaaga	ctcttggtca	tgaactgtct	cttcacaaag	caagtccacc	120
acttgctggg	tttatcattc	tgagggtcga	aaactttctc	acaaagtctc	agtccagtct	180
cttgcccttag	ctggttgtaaa	taggctctca	tcacttcatc	ttctgtttgt	ttgcaggttt	240
ggcataaatt	gcgttaagt	gaaaaccagg	ctctccagga	atgggaaaaat	taagtgttc	300
ccagcgtata	catttctttc	tcaccttggc	ttttggaatt	gcacttttgc	agtttcttca	360
nacattcaga	aatgtagaga	gttatatata	tcaangncct	atcaacttca	ttcttaattt	420
cataagtttt	gaaaaaaaca	ttggcccttg	aagtaataaa	tngntttatt	cccaaaatct	480
ggatcntttg	gcnctctnng	ggcangnccc	ttgaaatgac	ttttgatagg	gaacaangcc	540
ctggtttcca	nnagnttggg	ttcnggaccn	taaaaaaaaa	gggaanccgg	nttttggnng	600
gcccggttta	acccaagggc	cggancn				627

<210> 503
 <211> 629
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(629)
 <223> n = A,T,C or G

<400> 503						
ggtacattag	tagagctctc	caatcacagg	cagacgccag	tgtcctatga	ccagggggca	60
aatatggcca	aacagattgg	agcagctact	tatatcgaat	gctcagcttt	acagtcggaa	120
aatagcgtca	gagacatttt	tcacgttgcc	accttggcat	gtgtaaataa	gacaaataaa	180
aacgttaagc	ggaacaaatc	acagagagcc	acaaagcggg	tttcacacat	gcctagcaga	240
ccagaactct	cggcagttgc	lacggactta	cgaagggaca	aagcgaagag	ctgcaactgtg	300
atgtgaatct	ttcattatct	ttaatgaaga	caaagggaatc	tagtgtaaaa	aacaacagca	360
aacaaaaagg	tgaagtctaa	atgaagtgc	cagccaaagt	catgtatcca	gaggcttang	420
aggcgtttga	gangatactc	atcttttttg	aatnctgcct	taggttcggc	atgtanacca	480
agtgatgaga	agtgaatcca	tggaaagagt	ttaatgtgac	ttggaaaata	tgccaaaaaa	540
tgagagatcc	aataacttna	ggaaaataag	ggggatccaa	tncctncccg	gcggccctta	600
ggggaattca	aacactnngg	gcggtatan				629

<210> 504

<211> 462
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (1)...(462)
 <223> n = A,T,C or G

<400> 504
 acgcgggagc tgagtgtccc gcggggcccg aagcgtttac tttgaaaaaa ttagagtgtt 60
 caaagcaggc ccgagccgcc tggataccgc agctaggaat aatggaatag gaccgcggtt 120
 ctattttgtt ggttttcgga actgaggcca tga^ataagag ggacggcccg gggcattcgt 180
 attgcgcgcg tagagggttaa attcttggac cggcyc^aaaga cggaccagag cga^aaagcatt 240
 tgccaagaat gttttcatta atcaagaacg aaagtcggag gttcgaagac gatcagatac 300
 cgtcgtagtt ccgaccataa acgatgcccg accggcgatg cggcggcggtt attccatgac 360
 ccgncgggga gcttcgggga aaccaaagtc tttggttcc ngggggagta tnggtgcaaa 420
 aaaaaaaaaa aaaaaaaaaa gtcctnggnc gcgacccctt aa 462

<210> 505
 <211> 628
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(628)
 <223> n = A,T,C or G

<400> 505
 actttttttt tttttttttt tttgggggag gttatatggg tttaatagtt tttttaattt 60
 atttaggggg aatgatgggt gtctttggat atactacagc gatggctatt gaggagtatc 120
 ctgaggcatg ggggtcaggg gttgaggtct tggtagtgtt tttagtgggg ttagcgatgg 180
 aggtaggatt ggtgctgtgg gtgaaagant atgatggggt ggtggttgtg gtaaacctta 240
 atagtgtagg aagctgaata atttatgaag gagaggggtc aggggttgatt cgggaggatc 300
 ctattgggtg gggggctttg tatgattatg ggcgttgatt agtantaatt actggttgaa 360
 cattgtttgt tgggtgtatat attgnaattg agattgctcg ggggaatang ttatgtga^t 420
 aggaataggg ttangatgag tgggaagaaa aaaagaaagg aantaaaagt ttaattattc 480
 cctttttggg ttgaagngat natggaaggg gaaaatttgg gccttgaaat tgtttaagta 540
 atacttttct aataaggtaa gtctagaaga atagggcngg ttttggctct aaaaaggcta 600
 aaaggggatt ggcggggtgg atccnccc 628

<210> 506
 <211> 612
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(612)
 <223> n = A,T,C or G

<400> 506

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acggtagaac  tgcattatt  caccctatgt  gggtaattga  ggagtatgct  aagattttgc  60
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gtggggagaa  ggcttacgtt  cagtgaaggga  gagatttggt  atatgattga  gatgggggct  180
agtttttgtc  atgtgagaag  aagcaggccg  gatgtcagag  ggggtgcctt  ggtaacctct  240
gggactcaga  agtgaaagg  ggctattcct  agttttattg  ctatagccat  tatgattatt  300
aatgatgagt  attgattggt  agtattgggt  atgggttcatt  gccggagaag  tatattgttg  360
aagaggatag  ctattagaag  gattatggat  gccgttgctt  gcctgaagaa  atacttgatg  420
gcagcttctg  tggaaacca  gtttattttt  ttgntagaa  ctggaataaa  acctacatgt  480
ttatttctan  gccactcagg  taaaaaatca  tgcnaactta  acccttgata  atgtgcctcc  540
aaaatgtaaa  aaaataacgg  ttggcccg  ataatcccg  ncttgccga  cccctagg  600
aattcccccc  tg  612

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<210> 507

<211> 632

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(632)

<223> n = A,T,C or G

<400> 507

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ggtactacgt  tgtagccac  ttccactatg  tcctatcaat  aggagctgta  tttgccatca  60
taggaggctt  cttcactga  tttcccctat  tctcaggcta  caccctagac  caaacctacg  120
ccaaaatcca  tttcactatc  atattcatcg  gcgtaaatct  aactttcttc  ccacaacact  180
ttctcggcct  atccggaatg  ccccgacgtt  actcggacta  ccccgatgca  tacaccacat  240
gaaacatcct  atcatctgta  ggctcattca  tttctctaac  agcagtaata  ttaataattt  300
tcatgatttg  agaagccttc  gcttcgaagc  gaaaagtcct  aatagtagaa  gaaccctcca  360
taaacctgga  gtgactatat  ggatgcccc  caccctacca  cacattcgaa  gaaccctgat  420
acataaaatc  tagacaaaaa  aggaaggaat  cgaaccccc  aaactgggtt  nagccaaccc  480
catgggcttc  acgacttttt  tataaaaaaa  aaaaaaaaat  aaaagtcttg  gcccggnngg  540
cggtcanggn  gaaattcaac  nactggngg  cggctctaang  ggtccaactc  gggnccaacc  600
tgggggaaaa  tgggaaagt  gttcctgggg  aa  632

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<210> 508

<211> 336

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(336)

<223> n = A,T,C or G

<400> 508

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cggctcctta  atgctgctcn  cccggccgca  ntgtgattgg  atatcttgca  gaattcgccc  60
ttagcgtggt  cgccgggccc  aggtacaact  tccaaaaagg  agacattgga  gaanaaccaa  120
gctgggtcta  taaggaaatt  cacatgagat  ggcacacata  tttatgctgt  ctgaaggnga  180
cgatcatgtt  accatatcaa  gctgaaaatg  tcaccactat  ctggagattt  cgaccgtggt  240
ttcctctctg  aatctgttat  gaacacnttg  gttggctgga  ttcantaata  aatatgtaag  300
gcctttcttt  tcaaaaaaaa  aaaaaaaaaa  aaaagt  336

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<210> 509
 <211> 624
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(624)
 <223> n = A,T,C or G

<400> 509
 ggtacttttt tttttttttt ttttttttta tagatacaat tggcttttat ttgtgattca 60
 tgagtcaggg cagtttccat tctgcaaaat atagtgatag ctctactgg gcaatacaac 120
 agtanaacag tgggttttgt aaaatgggaa tccaggaaca gaagaatata aataaattga 180
 tttaaataaa ctgattgggt aatttcagaa tacttcatat tacttttttc taagagttaa 240
 agcagaaagg actttcttac tgtgctgact canacagcct ggactctcat gtttttagga 300
 aaattttgct gttctgggat ctacctgctt cctcatgttt cagtngagat atatggcatt 360
 taacatgact ggctccattc tggagtccca ggctgtccct aaatgagaag ttgactaaac 420
 ataaggnatt aacactactg ncaggtagca tcattttggc ttncatcatt catanggtat 480
 gatgnccnc naatcatacc tttatttgag tttttgncat tccnncccaa aaaaaaatt 540
 ttgaanttta ccaaaggntg catgccacnt ttaaagggtt anaaaatcnc cccnccnggn 600
 actaatnttg ggccatcngn nggc 624

<210> 510
 <211> 619
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(619)
 <223> n = A,T,C or G

<400> 510
 acggatgcta cttgtccaat gatggtaaaa gggtagctta ctggttgctc tccgattcac 60
 gttagaatga ggaggtctgc ggctaggagt caataaagt attggcttag tgggcgaaat 120
 attatgcttt gttgtttgga tatatggagg atggggatta ttgctaggat gaggatggat 180
 agtaataggg caaggacgcc tcttagtttg ttaggacgg atcggagaat tgtgtaggcc 240
 aataggaaat atcattcggg cttgatgtgg ggaggggtgt ttaanggggt ggctagggta 300
 taattgtctg ggtcccctaa gaggtctggt gagaatagt ttaatgtcat taangagaga 360
 aagaaaaaaa ataagcccga gggcgtcttt gattgtgtan taaagggtga angtgatttt 420
 atcngaattg gaagtgattn ctaaggggtt ggtttgatcc ctttcgtgcc aaaataagaa 480
 gnggaatgct gctagggtc cataatgaag gcaanataaa atgaaagnaa aaaatctgta 540
 aggnnggact gctactaata ncctcccaa tcttgaacaa gntttncaa ttntggatgy 600
 nggtataant tnaattcnn 619

<210> 511
 <211> 634
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature

<222> (1) ... (634)

<223> n = A,T,C or G

<400> 511

cgaggacgcg	gggagatggc	ctagaagcaa	tgatagccat	cactgagaac	acctagcacc	60
caatcttggg	tcctaatacc	attctcccat	caaaggaacc	agagatcctt	ggagaaatgg	120
ttaaggaaatg	aggcaggaaa	tatacaagat	aagcctggag	catcttatag	ctctagaaag	180
taagaaagta	cctgcctatt	ttagaatcct	agagaacatt	tcattgtaag	aaactagccc	240
attattttaag	tgtccacagt	atctttcatt	tcagtgggtcc	aagatgcgaa	ggtttccaga	300
cacaatcttg	ttctctaata	ctgctccagg	tgggatatca	attctgtccc	catgatttgc	360
aatgatgata	cccgttcctt	ttaatgaaac	atcttttnc	aatgtcacat	cttctgaaac	420
tgngaggnga	tccaattcaa	gcataatctg	gntactttcc	aaatcctctt	agataatctt	480
gaaccttcgt	aaaagaactg	gctaattaan	ccanggccct	gnaggaaatt	ccccttttcc	540
tcattggcag	anancctgca	ttaaantntt	aagggttgnn	ttncnccan	aaactgtgtg	600
gtttgnaggc	aaaaaacggt	cttgggcatt	ancc			634

<210> 512

<211> 623

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1) ... (623)

<223> n = A,T,C or G

<400> 512

ggtagcgagg	cattgttcat	gactttaaca	agaaacttac	agcctattta	gatcttaacc	60
tggataaagt	ctatgtgatc	cctctgaaca	cttccattgt	tatgccaccc	agaaacctac	120
tggagttact	tattaacatc	aaggctggaa	cctattttgc	tcagtcctat	ctgattcatg	180
agcacatggg	tattactgat	cgcattgaaa	acattgatca	cctgggtttc	tttatttatc	240
gactgtgtca	tgacaaggaa	acttacaaac	tgcaacgcag	agaaaactatt	aaaggtattc	300
agaaacgtga	agccagcaat	tgtttcgcaa	ttcggcattt	tgaaaacaaa	tttgccgtgg	360
aaactttaat	ttgtcttgaa	cagtcaagaa	aaacattatt	gaggaaaatt	aatatcacag	420
catacccccc	cctttacatt	tgngcagng	gatatttttt	aaagcttctt	tnatgtaagt	480
agcaacangg	ntttactatc	tttcatttca	taaatcaatt	aaancnttnc	ctcaaaaaaa	540
aaaaaaaaaa	aaaaatacct	ncccggcggc	gctccaaagg	ggaattcaan	caccgngggc	600
cgtcttttggg	accaacncgg	gcc				623

<210> 513

<211> 623

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1) ... (623)

<223> n = A,T,C or G

<400> 513

actgccctct	ccagatcagc	agttcaggag	agcacaggag	gcaaaacaca	gattgctggg	60
cttattgggtg	ccatcatcgt	gctgattgtc	gttctagcca	ttggatttct	cctggcacct	120
ctacaaaagt	ccgtcctggc	agcttttagca	ttgggaaact	taaagggaat	gctgatgcag	180

tttgetgaaa	taggcagatt	gtggcgaaa	gacaaatatg	attgtttaat	ttggatcatg	240
accttcatct	tcaccattgt	cctgggactc	gggttaggcc	tggcagctag	tgtggcattt	300
caactgctaa	ccatcgtgtt	caggacccaa	tttccaaaat	gcagcacgct	ggctaataatt	360
ggaagaacca	acatctataa	gaataaaaaa	gattattatg	atatgtatga	gccagaagga	420
gtgaaaattt	cagatgtcca	tcttctatct	actttgcnaa	cattggnttc	tttaggcngg	480
aacttatcga	tgctggtnng	ctttagtnc	ctttgnaatt	tacgcaagcc	ccacaaactt	540
tgaggaaatc	ccaaactgcn	aancangntt	nttcagtgg	acccaanggt	tttttttcct	600
tgggccgacn	ccctangna	atn				623

<210> 514
 <211> 627
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(627)
 <223> n = A,T,C or G

<400> 514						
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ttgatccgca	tcaatgatgg	gggtcggcca	cccttgggaag	gcattgtttc	tttaccagtt	120
acattctgca	gttgtgtgga	aggaagtgtt	ttccggccag	caggtcacca	gactgggata	180
cccactgtgg	gcatggcagt	tggtatactg	ctgaccaccc	ttctggtgat	tggtataatt	240
ttagcagttg	tgtttatccg	cataaagaag	gataaaggca	aagataatgt	tgaagtgtct	300
caagcatctg	aagtcaaacc	tctgagaagc	tgaatttgaa	aaggaatgtt	tgaatttata	360
tagcaagtgc	tatttcagca	acaaccatct	catcctatta	cttttcatct	aacgtgcatt	420
ataatttttt	aaacagatat	tccctcttgt	cctttaatat	ttgctaaata	tttctttttt	480
gangnggagt	cttgctctgt	cgncacaagt	ggantacctg	ncccggccgg	ccgtcaaagg	540
cgaattcaac	aactggcggc	cgtactaatg	gatcgacctc	ggaccaactt	ggggaacatg	600
gcanactngt	tcctgngnaa	aggatcc				627

<210> 515
 <211> 605
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(605)
 <223> n = A,T,C or G

<400> 515						
accattgggtg	gccaatgtgat	ttgatggtaa	gggagggatc	gttgacctcg	tctgttatgt	60
aaaggatgcc	gtanggatgg	gagggcgatg	aggactagga	tgatggcggg	caggatagtt	120
cagacgggtt	ctatttcctg	agcgtctgag	atgttagtat	tagttaagtt	ttgttgtgag	180
tgtaggaaa	aggcataca	ggactaggaa	gcagataagg	aaaatgatta	tgagggccgt	240
gatcatgaaa	ggtgataagc	tcttctatga	taggggaaaag	taancgtctt	gtanacctac	300
ttgcgctgca	tgtgccatcc	cgccgtaccc	taacccgtgc	aaaggtagca	taatcacttg	360
ttccttaatt	aagggaacctg	tatgaatggc	ttcaccaggg	ttcaactgtc	tcttactttt	420
aaccagtga	attgacctgc	cctgaanag	gcggcgttac	acaccagacg	agaaaacctt	480
tgagagctaa	ttattatcca	acatacctng	ccggaccccc	taaggcgaat	tccaccactt	540
gcggcgtcta	tgatccact	cggaccactt	ggggaaaagg	ctactgtcct	ggnaatgttt	600

cctcn

605

<210> 516
 <211> 464
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (1)...(464)
 <223> n = A,T,C or G

<400> 516
 ggtacaacta atccgtgaca aattaccaga ttaattttac tttattttctt caggcctggg 60
 gttttttcgat gagttcaa at ttgggatctt caaatttgaa ggtgggaaat gtattcatgt 120
 ctgcattacc aaacatttgc ttgagcttaa aaagctccct ctccagctct tgctgatact 180
 ctgaactagc atcaacaggt cctccagatg tctgttgctt agatttgat tctctaactct 240
 tgtccacaaa gagtttctgt ataggatcaa gttccttatt aaatgccact gctgtaacac 300
 caatgttcct ccgcaaatgg actgagacgg ctgaccgaat gacagaggag aacctgaaga 360
 gcctctgaag aatcatgctg attccttgac tcagtcccga gctgncaaag ccttcgccgc 420
 caccaccttc gntctacccc cgcgtacctg cccggcgggc gctc 464

<210> 517
 <211> 611
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (1)...(611)
 <223> n = A,T,C or G

<400> 517
 acccggagca cggagatctc gccggcttta cgttcacctc ggtgtctgca gcaccctccg 60
 cttcctctcc taggcgacga gaccagtggt ctagaagttc accatgtcta ttctcaagat 120
 ccatgccagg gagatctttg actctcgcag gaatcccact gttgaggttg atctcttcac 180
 ctcaaaaggt ctcttcagag ctgctgtgcc cagtgggtgt tcaactggta tctatgaggc 240
 cctagagctc cgggacaatg ataagactcg ctatatgggg aagggtgtct caaaggctgt 300
 tgagcacatc aataaaaacta ttgcgcctgc cctgggttagc aagaaactga acgtcacaga 360
 acaagagaag attgacaaac tgatgatcga gatggatgga acagaaaata aatctaagtt 420
 tgggtgcgaac gccattctgg ggggtgtcctt tgccgtctgc naaactgggt ccgttgagaa 480
 ggggggtccc tgtccttggc cggacacnct aaggcgaatt ccacacactg cggccgtact 540
 atggatcgac tcggnaccaa cttgggtaat atgggcatac tggtnctggn gaaatgtttc 600
 cctccaatcc a 611

<210> 518
 <211> 435
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (1)...(435)

<223> n = A,T,C or G

<400> 518

cgaggtactt	tntttttttt	tttttttttt	ttttaagagg	aaaacccggt	aatgatgtcg	60
gggttgaggg	ataggaggag	aatgggggat	aggtgtatga	acatgagggt	gttttctcgt	120
gtgaatgagg	gttttatgtt	gttaatgtgg	tgggtgagtg	agccccattg	tgttgtggta	180
aatatgtaga	gggagtatag	ggctgtgact	agtatgttga	gtcctgtaag	taggagagtg	240
atatttgatc	aggagaacgt	ggttactagc	acagagagtt	ctcccagtag	gttaatagtg	300
gggggttaagg	cgaggttagc	gaggcttgct	agaagtcac	aaaaagctat	tagtgggagt	360
aga-gtttgaa	gtccttgaaa	gaggattatg	atgccactgt	gaatgccttc	ctagtgtgag	420
tttgctagcc	cgcgt					435

<210> 519

<211> 407

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(407)

<223> n = A,T,C or G

<400> 519

actttntttt	tttttttttt	tttttttttt	ncagctttgc	aaccatactc	cccccggaac	60
ccaaagactt	tggtttcccg	gaagctgccc	ggcgggtcat	gggaataacg	ccgccgcac	120
gccggtcggc	atcgtttatg	gtcggaacta	cnacggtntn	tgatcgtnnt	cnaacctccg	180
actttcgttc	ttgattaatg	aaaacattct	tggcaaatgc	tttcgctctg	gtccgtnntg	240
cgccgggtcca	anaatttcac	ctctagcggc	gcaatacnaa	tgcccccggc	cgccccctct	300
aatcatggcc	tcagttccga	aaaccaacaa	aataaaaccg	cggtcctatt	ccattatgcc	360
tagctgcggg	atccaggcgg	tccccgggtac	ctnggccgng	accacgc		407

<210> 520

<211> 613

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(613)

<223> n = A,T,C or G

<400> 520

accttctggg	gcatacaaca	tggcagcagg	gcctcgggaa	gaggggtagg	aggaccgagc	60
agcattctct	gtagaggag	acaggaaagg	agacccctct	ggcacacatt	tatggagggg	120
tgtccctgaa	gagaagggca	ggtgggagag	gttccctgtt	acttaagaga	aggcaccagt	180
ggcaaagagc	acaatgaaga	ggatgatgat	aaaaacaatc	acgcagataa	ggacaatcat	240
cttcacgttc	ttccaccaga	attttcgagc	caccttctgc	gatgtcgtct	tgaagtgtct	300
agatgtgggt	tccagatcct	ctgtcttggt	gcggagatgt	tccaagtttt	ccccccgggc	360
caggatccgc	tccacattct	gggtcataat	attcttaact	ccctccacct	cactttgcag	420
gttcgcgaca	cgatcatttc	cttcaccttc	actggcttnc	tncatgtctc	aaagcaccca	480
gccggcagta	agtgaatcgc	ctatcggntt	cttccaggng	ggcctanttn	anttctgggtg	540
gtcaactttc	ccgcgcgtact	tgggcggacc	ccctaagggg	aattcactgg	cggccgtctt	600
tggatccacc	cgn					613

<210> 521
 <211> 606
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(606)
 <223> n = A,T,C or G

<400> 521
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 catgtcaatg gatatggaaa gataactggc aaaaatcaag tcaactgctac gaaagctgat 120
 ggccggcactc aggttattga taaaaagaac attcttatag ccacgggttc agaagttact 180
 ccttttctcg gaatcacgat agatgaagat acaatagtgt catctacagg tgctttatct 240
 ttaaaaaaaag ttccagaaaa gatggttggt attggtgcag gagtaatagg tgtagaattg 300
 ggttcagttt ggcaaaagact tgggtgcagat gtgacagcag ttgaattttt angtcagtga 360
 ggtggagttg gaattgatat ggagatatct aaaaactttc aacgcatacct tcaaaaaacag 420
 ggggtttaaat ttaaattgaa tacaanggta ctggtgctcc aagaagcana tggaaaaatt 480
 gatgttctat tgaanctctt ttgngggaaa gctgaantnt acttggatgn cctnggccgn 540
 acncnctagg caatccncca ctggngccnt ntttggtecn cctgggtccaa ctgggnnann 600
 nggctn 606

<210> 522
 <211> 617
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(617)
 <223> n = A,T,C or G

<400> 522
 acttgcgctt actttgtagc cttcatcagg gtttgcagaa gatggcggtg tataggctga 60
 gcaagaggtg gtgaggttga tcgggggttta tcgattacag aacaggctcc tctagagggg 120
 tatgaagcac cgccagggtcc tttgagtttt aagctgtggc tcgtagtggt ctggcgagca 180
 gttttgttga ttttaactgtt gaggttttagg gctaagcata gtgggggtatc taatcccagt 240
 ttgggtctta gctattgtgt gttcagatat gttaaagcca ctttcgtagt ctattttgtg 300
 tcaactggag ttttttaciaa ctcanagtga ttttagcttt attggggagg ggggtgatcta 360
 aaacactctt tacgccggct tctattgact tgggttaatc gtgtgacctg cgggtggctgg 420
 cacgaaattg accaaccttg gggtttagtat aacttaatta aactttcntt attgctnaag 480
 gtaatcctgg tggttncctt gggggngtng ntaggctaaa cgtttgaacc tcattctgcy 540
 gcctganctt ggccctttta tcgggggatt aaaaggggac tncctgaach gggngcttct 600
 tggnaaatta taaaaca 617

<210> 523
 <211> 608
 <212> DNA
 <213> Homo sapiens

<220>

<221> misc_feature
 <222> (1)...(608)
 <223> n = A,T,C or G

<400> 523

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ttttgcaaat	aaaactggct	aagttgggtg	ctttttgggtg	attaagtcaa	aganaccaaa	120
tcccatatcc	tcgtccgact	cctccgactc	ttccttggct	tcaaccttan	ctggggctgc	180
agcagcagca	ggagcagctg	tgggtgtagc	aaccacaggg	gcagcancca	caaaggcaga	240
tggatcaacc	aanaaggcct	tgaccttttc	aacaagtggg	aaggngtaat	ccgtctccca	300
aacaaagtca	ggactcgttt	gtctcttcaa	aaaaaaaaag	cganggctcg	catttggtcc	360
cctttggaca	ttttgcaact	cttcaatggg	gttncattgg	tnggtgatgg	tataaacctt	420
tgangnacct	gcccggccgg	ccgtcaaang	gcaaattcac	ccactggcgg	ccgttctatg	480
gatccnacc	ggncccaact	tgggtaatat	ggcanactgt	tcctggggga	aatgtntccc	540
tnaaattccc	acaaanacaa	nccgaaccta	aangtaancn	gggggccaag	agggcnaccn	600
ccttattg						608

<210> 524
 <211> 398
 <212> DNA
 <213> Homo sapiens

<400> 524

ggtacaggat	cctctaaaga	gaccgcctgg	ctgggtgctc	aaaccacatg	ggccgaccca	60
aaagacgtca	aaaccaagag	ctgctcagga	ggcactaaat	gttgacggtc	ttggccggct	120
tcacatcttc	aatttcagca	gacagccagc	ggtaagtgcg	atgacgccgc	agcacctcaa	180
tggccttgag	ttccagtgg	gttgctgaa	taccaagggtc	ttctaagcca	ggcagggtgag	240
gcaatttcat	gtctgtgatg	tgcattccgt	ccactttatc	ccttggtatc	cagggctcaa	300
atgggcttat	ttcaaagact	cttgctaccc	atcgataggc	aaaaagcggc	aaggggaatg	360
ggaggaacaa	tctgtgagcc	acaacaaaga	tgtacctg			398

<210> 525
 <211> 607
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(607)
 <223> n = A,T,C or G

<400> 525

actgttctctg	ttggcccag	tggagactgg	tgttctcaaa	cccggtatgg	tggtcacctt	60
tgctccagtc	aacgttacaa	cggaagtaaa	atcgtcgaa	atgcaccatg	aagctttgag	120
tgaagctctt	cctggggaca	atgtgggctt	caatgtcaag	aatgtgtctg	tcaaggatgt	180
tcgtcgtggc	aaccgttgct	ggtgacagca	aaaatgacct	accaatggaa	gcagctggct	240
tactgtctca	ggtgattatc	ctgaaccatc	caggccaaat	aagcgccggc	tatgcccctg	300
tattggattg	ccacacggct	cacattgcat	gcaagtttgc	tgagctgaag	gaaaagattg	360
atcgccgttc	tggtaaaaag	ctggaaaaatg	gccctaaatt	cttgaaatct	ggtgatgctg	420
ccattgggtga	tatgggtcct	ggcaagccca	tgtgtgtttg	agagcttctc	aaactattca	480
ccttgggtcc	tttgcgtcgc	tgatatgaaa	aaacagtgcg	ggggtgtatc	aaacatggac	540
aaaagnttnt	tgacttgacg	gtaccaattt	nccaaaacta	aaaggtnaan	aaatttncca	600
aaccgcc						607

<210> 526
 <211> 624
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(624)
 <223> n = A,T,C or G

<400> 526
 cgaggtacgc gggggaagct ctgtttggtg ctttggatcc atttccatcg gtccttacag 60
 ccgctcgtca gactccagca gccaaagatgg tgaagcagat cgagagcaag actgcttttc 120
 aggaagcctt ggacgctgca ggtgataaac ttgtagtagt tgactttctca gccacgtggt 180
 gtgggccttg caaaatgatc aagccttttct ttcattccct ctctgaaaag tattccaacg 240
 tgatattcct tgaagtagat gtggatgact gtcaggatgt tgcttcagag tgtgaagtca 300
 aatgcacgcc aacattccag ttttttaaga agggacaaaa ggtgggtgaa ttttctggag 360
 ccaataagga aaagcttgaa gccaccatta atgaattagt ctaatcatgt tttctgaaaa 420
 tataaccagc ccattggcta tttaaaactt gtaatttttt taatttacca aaatntaaaa 480
 tntgaagacn taaccagtt gncatctgcg tgacaatnaa acattaatgc tacactttta 540
 aaaaaaaaaa aaaaaaaaaa gtcctgccng cggccctcaa aggggaattc cacacctggg 600
 ggccgtcttt nggncccacc cgnn 624

<210> 527
 <211> 611
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(611)
 <223> n = A,T,C or G

<400> 527
 acagagtgc actgaacaga tcacaaagca cgagaaacat tagttctctc cctccccagc 60
 gtctccttcg tctccctggg tttccgatgt ccacagagtg agattgtccc taagtaactg 120
 catgatcaga gtgctgtctt tataagactc ttcattcagc gtatccaatt cagcaattgc 180
 ttcacaaat gccgtttttg ccaggctaca ggcccttttc ggagagtta gaatctcata 240
 gtaaaagact gagaaat*ta gtgccagacc aagacgaatt ggggtgtgtag gctgcatttc 300
 tttcttacta atttcaaatg ctccctggta agcctgctgg gaggtcgaca cagtggtttg 360
 tttgttgctc cagatgccac ttcagaaaga tcctaaaata atctcctttc attttcaagt 420
 agaacacctt actttctggg tgtgtagcat tgggaataaa atatttgtcc acagcttcag 480
 aacatcattg cagatgtctt gcagtctggc tntatctttt acggnacctc ggccgggaca 540
 ccctanggcg aattccacac ctggcggcgg tctantggac ngctnggcca cttgggnana 600
 tggctactgt t 611

<210> 528
 <211> 615
 <212> DNA
 <213> Homo sapiens

<220>

<221> misc_feature
 <222> (1)...(615)
 <223> n = A,T,C or G

<400> 528
 ggtacttttt tttttttttt ttttttttga gacggagtct tgttcagctg cccaggctgg 60
 agtgcagtgg ctcgatcttc gctcactgca accaccgtct cctgggttca agcgattctc 120
 ctgtctcagc ctcccaagta gctgggatta caggccacca ccatcatgcc cggctaattt 180
 ttgtatattg gtagagacgg agtttcacta tgttgggcag gctggtcttg aactcctcac 240
 ctccaggtgat ccgcccgtct tggcctccca aagtgcagg attacaggcg taagccacca 300
 tgccctggcca gatgatgtat ttaaataatca taccaaactc tgtgtattta tataaagaaa 360
 gactggtaaa agacttcctn attttaaaaa aaaccaaacc ccaaaccaaa aaaaacttta 420
 cccttaccat tgntgcata tgtgcagtat aaaacacaca cttattngga catganaaaa 480
 ccgnaagaaa gncccgggta aactggactt tgccgccttt aaaaataaaa tcnaataagn 540
 gccttgaggg cctttttcaa tgcaattttt taaccgggac ctgccnggng gcggttaaggg 600
 naatccanctn ctggn 615

<210> 529
 <211> 352
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(352)
 <223> n = A,T,C or G

<400> 529
 cgaggtaact tntttttttt tttttttttt tttttgggaa aagtcatgga ggccatgggg 60
 ttggcttgaa accagctttg ggggggttcga ttccttcctt ttttgtctan attttatgta 120
 tacgggttct tcgaatgtgt ggtagggttg ggggcatcca tatagtcact ccaggtttat 180
 ggagggttct tctactatta ggacttttcg cttcgaagcg aaggcttctc aaatcatgaa 240
 aattattaat attactgctg ttagagaaat gaatgagcct acagatgata ggatgtttca 300
 tgtggtgtat gcatcggggt agtccgagta acgtcggggc attccccgc gt 352

<210> 530
 <211> 769
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(769)
 <223> n = A,T,C or G

<400> 530
 ggtactgcat agattaaaga aataaaactgc agtaaagcca ctcgtaagga atgaacgcc 60
 ttgccaatga taatcctctg cacataggtg gaaatagcaa agaagtatag ttgcttcaga 120
 acaggtaata accaaaatga taaacaccag aaataggaag ccaaaccatgt aatacatctg 180
 gtgtgaccaa atactattca gaatgaagaa aagttgtata aagatgcagc caaagggcaa 240
 aatccctccc atgataatac caggcaagggt cttcgtgtag aacgactgtt cagggaatctg 300
 acngtggaat ctgattggtt cgaactgggt gttcaatggc atcttcttaa aaccaangta 360
 tgcaccaata aacgtcnnag gcacagatat gtanacaaa gggccaatat ggcaancagt 420

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gtncccaaaa gaaatactgt tgganatect ctncccagag gtcagattnt tattaagaat 480
cnccecgegt cttttttttg tttttttttt gctccacttt nnggtaaaann acntttnttt 540
aaaaatgttt aantctantt cctaattccc atnttctttt gctncnnnnc tgctggnggn 600
ctttaaggga antcncnntt ggnggcgtcn atganccact tgnnactggn tantagcnac 660
gttcggggang tcccnctntt ctaatatccg gnagtaannc ggctttgncn cctantgggn 720
cngcttttcg aacntgcctn anannntccg gaggtgtatn ttcttctnn 769

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<210> 531
 <211> 777
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(777)
 <223> n = A,T,C or G

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<400> 531
cgaggtactt tttttttttt tttttttttt tgtttttttt tttttttctt cagctaaaac 60
agcgggaagag gtgatttatt atatggttgt tacactcggc cacaaataaa cacagaaata 120
gtccanaatg tcacaggtcc aggacagagg accaacatgg gcatttttgt tatgagcaag 180
gtgggtctna naggtgatcg gcgatcagag ggcgatgaag ttctagatcc attgagacaa 240
gctctagaca gtagcatgca gtcccacaac ttgtctccaa agattcaggt ttactcacgt 300
catccagcan agaatggaaa gtcaaatttc ctgaattgct atgtgtctgg gtttcatcca 360
tccgacattg aagttgactt actgaanaat ggagagagaa ttgaaaaant nggacattca 420
taactgnntt tcancaagga ctggtctttc tatctcttgg ncttntttt tcttntattt 480
ttttntaca tngggcctta ctttaaaaaac atacntttcc nnnttacnctn tggatgccaa 540
tngatttcna nanatttccn agnggaatcc tttngttatt nttaaaantt gggatctntn 600
gccancactt ggctaantnt taccncttt nggaatngtc ntatgntcat tnttggaaat 660
tnccccctn angnntttct ttngngnta aaaattntta atnnttaa at tntttttcna 720
anattnttca aatactaana ntntnnggg nttanannaa tntgtanat gggnnng 777

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<210> 532
 <211> 764
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(764)
 <223> n = A,T,C or G

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<400> 532
actttacaag atagattgta taagaagcca aataatgaaa gcctagaaaa aactaattta 60
tacttatctg aaggttacaa attagacttt taaattttct ttgtagttgg tgggtgttga 120
gggttggtta gaaatgaaag cctggatttt gtgccatggt tgtaatatag tttgttcctt 180
gatcaaataa tcagagaaaa gaaacttaaa gatctttgtc tgtgaagaag aaaattatct 240
ccctagtcca atctgtagtg aaataagact acagaaggca ttgttttttc ctttttattt 300
tntgnattat atatttttct taaatatggt ttattgtctt ctctaagcaa aaagtcttta 360
ataaacatag tatttctctc tgcgtcctat ttcattagtg aagacatagt tcacctaaaa 420
tggtatnctg ctctgaatct agctttttat aaatggctat gtttttgatg atatgtcaca 480
ttcaaaatgg cctaattaaa tgtgttaaat gnaatggcac tcttataacc ttaaaataac 540
canaattaac cctccaaaaa aanaaaaaaa aaaaaggcct tggccgacnc ntangngant 600

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caccnctgng	gcntcatgga	cncttgccca	cttgngaann	nggtnangnt	ccggganatt	660
tccccatncc	aattcancgg	acatagnnac	cnggccnaag	ngnnccantg	nngnnnnnct	720
tnnngaacng	gccctnaacn	cccggggngg	tngttcnccc	tcnc		764

<210> 533
 <211> 773
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(773)
 <223> n - A,T,C or G

<400> 533						
cgagggtactt	tttttttttt	ttttacagat	acaattggct	tttattttgtg	attcatgagt	60
cagggcagtt	tccattctgc	aaaatatagt	gatatctcct	actgggcaat	acaacagtag	120
aacagtgggt	tttgtaaaat	gggaatccag	gaacagaaga	atataaataa	attgatttaa	180
ataaactgat	tgggttaatt	cagaataact	catattactt	ttttctaaga	gttaaagcag	240
aaaggacttt	cttactgtgc	tgactcagac	agcctggact	ctcatgtttt	taggaaaatt	300
ttgtctgttc	tgggatctac	ctgcttcctc	atgttcagt	tgagtatatg	gcatttagca	360
tgactgggtcc	attctggagt	caccaggctt	gcacctaaat	gagagttgac	taancatagg	420
cnttaacact	actgcagtag	catcatttng	acttcatcat	catanggtat	gatgncntct	480
aatnttncat	tatttgagtt	tggcattcag	ccacgagaga	atattgcctt	tgacaatgnt	540
gcattgcaact	ttaaagggtt	tagatncgcc	nccnggnact	atttnggaaa	tcgggggtcc	600
cccnanttgg	agtttnacct	ggcngaccnn	tgacnaccat	taaggantgt	tagantnccc	660
ttgaaccccc	tttacacct	ttgnatttcc	cggcntaacc	ccgggcnnnta	agggatccnt	720
tggcntnnng	ccngcnatn	gaagnacntt	ngannacgcc	tcncaccan	nng	773

<210> 534
 <211> 730
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(730)
 <223> n = A,T,C or G

<400> 534						
acacagacaa	atztatgcga	ccagggcgaga	ggctgtagat	gattcatatt	tccaattggg	60
agggaggact	cgcttggtct	tataatatcg	agccaaacgg	tgaatccggc	tctctattag	120
aatcagacgg	aatttagcat	ccttatecct	tctgttcctc	tcaagatgct	ttcgaacagc	180
aactgctttc	ttaattaaat	ggtagagatc	ttcaggaaga	tcaggagcaa	gtcccttaga	240
cttaagaatt	cttaaaattt	tattgcctgt	cacaaaacgt	acaaattgac	caggctgttg	300
acggctgcct	ccacgtcggg	ggaataatc	tgacgaatct	gggagctcat	ggttgggttg	360
caagaaggag	ctaccacaaa	aacngtgctg	caggtccaga	agcaggagat	ggccgaaaaa	420
tgccccgaag	ttcaaccgag	aggaaatcga	ggcgcccgag	cttgaagaag	tcccgatgtg	480
tcgtcaacct	gtgaacagaa	caacccccga	ccgcnantgc	ccggtinctg	ccggacacct	540
anggggaatcn	accctgnggc	gtctangacc	acttgcccaa	ctggganntg	gaaatntccg	600
ggaaaagntcn	tcaatcccaa	ttaccgacna	agaactgggc	naagggtcnc	atatgggcnc	660
gccttnnnga	nctnccctta	annccccgga	gggtgntggg	tctcntctan	nntnnngtgg	720
nggnaaanag						730

<210> 535
 <211> 809
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(809)
 <223> n = A,T,C or G

<400> 535
 gcgtgggtcng cggccgaggt accaactgca gagccaggaa aactttgaag ccttcatgaa 60
 ggcaatcgggt ctgccggaag agctcatcca gaaggggaag gatgtcaagg ggggtgtcga 120
 aatcgtgcag aatgggaagc acttcaagtt caccatcacc gctgggtcca aagtgatcca 180
 aaacgaattc acggtggggg aggaatgtga gctggagaca atgacagggg ataaagtcaa 240
 gacagtgggt canttgggaag gtgacaataa actggtgaca actttcaaaa acatcaagtc 300
 tgtgaccgaa ctcaacggng acataatcac caataccatg acattgggtg acattgtctt 360
 caagagaatc agcangagaa tttaaacaag tctgcatttc atattatatt antgntgtaa 420
 aattaatgta attaaagtga actttgttta aaaaaagann nntnntntaa atanaaaaaa 480
 gtnccctgct ggcggccggt caaaggccaa ttccagcnac tngnggccnt actagtgatc 540
 nactcgtcna acttgcgtaa nntggcatac ttgttctnng taaatntatc cctcncatcn 600
 ccaaattcnn ccgagcttaa atntaaactg gggcctatag gnncaactct tttgggttgc 660
 ctgccntttn acgaacttcg ncccttttat antgcccccc ganagggtn gttggctttc 720
 ntnntatatt ctctctctcc ttgnngggtt ttanggtngg tcatntgggn tctntanttt 780
 agcttngaant ntantngntn tttntntnt 809

<210> 536
 <211> 755
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(755)
 <223> n = A,T,C or G

<400> 536
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 tgagggatag gaggagaatg ggggataggt gtatgaacat gaggggtgtt tctcgtgtga 120
 atgagggttt tatgttggtta atgtgggtgg tgagttagcc ccattgtgtt gtggtaaata 180
 tgtagaggga gtatagggtt gtgactagta tgttgagtcc tgtaagtagg agagtgtat 240
 ttgatcagga gaacgtggtt actagcacag agaattctcc cagtaggtta atagtggggg 300
 gtaaggcgag gtttagcgagg cttgctagaa gtcatacaaaa agctattant gggagtanag 360
 tttgaagtcc ttgagagagg attatgatgc nacttgtaat gcnttcgant ttgagtttgc 420
 tagcngaata nnatgaggat gtantccng gccaatatna aaatactccc cgtnaacttn 480
 aggggttnga taaaatgctg tctaccnng actttgccgn acaccttagg caattcanca 540
 ctggngccgt ctnanggncc cacttggnc acnttggnga acatggcnn ngctcntngga 600
 aatgtttcnt caattccnc ttcnaccgan tantgnaach ggggcanaag cncccatn 660
 gtccctccct tctngaactt nncnttaaa tcccccgga gggtnatgg cttctctcnc 720
 taananntnt tnnnggnnt tcnataanna taann 755

<210> 537

<211> 794
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(794)
 <223> n = A,T,C or G

<400> 537

cgagggtacga	aaggggacaag	agaaataaag	cctacttcac	aaagcgccctt	cccccgtaaa	60
tgatatcatc	tcaacttagt	attataccca	caccacacca	agaacagggt	ttgttaaaaa	120
aaaaaaaaaaa	aaaaaaaaaa	aaaaaagta	cttgactttg	ttcacagcat	gtagggtgat	180
gagcactcac	aattgttgac	taaaatgctg	cttttaaaac	ataggaaagt	agaatgggtg	240
agtgc aaatc	catagcacia	gataaaattga	gctagttaag	gcaaatcagg	taaaatagtc	300
atgattctat	gtaatgtaaa	ccagaaaaaa	taaatgttca	tgatttcaag	atgttatatt	360
aaagaaaaac	tttaaaaatt	attatatatt	tatagcaaaa	gttatcttaa	atatgaattc	420
tgttgttaatt	taatgctttt	gaatacacag	acntaaatga	agtattatct	gtaaaaatgt	480
atattagagt	tgtgatacag	agtatatatt	attcanccat	nttcatacta	ataatatgga	540
tttaaanata	tcctataaat	tcnaattcaa	nanaaannt	gntananaan	aanggnctgn	600
cggcggcgcga	nggcaattca	acaatgnngc	gtctanggac	nactgggtcca	cttggggaana	660
ggcaacttnc	tgggaatgat	ccttcattcc	canntaccna	gctanttaac	nggggcaaag	720
ggcccnntta	tgggnntngc	ntntnnaant	tgcccttaaa	accccggnng	gtgntggntc	780
tttnnttttn	ngnt					794

<210> 538
 <211> 766
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(766)
 <223> n = A,T,C or G

<400> 538

ggtacgcggg	ggaaggccctt	ccttttttctg	ctgggctgcc	aacatgccat	ccagactgag	60
gaagacccgg	aaacttaggg	gccacgtgag	ccacggccac	ggccgcatag	gcaagcaccy	120
gaagaccccc	ggcgccgcg	gtaatgctgg	tggtctgcat	caccaccgga	tcaacttcga	180
caaataccac	ccaggctact	ttgggaaagt	tggtatgaag	cattaccact	taaagaggaa	240
ccagagcttc	tgcccaactg	tcaaccttga	caaattgtgg	acttttgtca	gtgaacagac	300
acgggtgaat	gctgctaaaa	acaagactgg	ggctgtccca	tcattgatgt	ggtgcgatcg	360
gctactacaa	agttctggga	aggggaaagc	tccaaagcaa	nctgtcatcg	tgaaggccaa	420
atcttcacag	aagagctgag	gagaaaaata	agantgttgg	ggggcctgtg	tctggtgctt	480
gaagcccat	ganggagttt	aattaatgct	actcttttga	aaaaaanann	aananaaaaa	540
gacctgccc	gcggcngtaa	ggcaattcac	cnttgnngcc	tctaaggacc	actggccaan	600
tgggaanang	gcnaanntcc	tgggaatngt	tentcaattc	cccaattaac	caanaangna	660
acnngggcca	nnnggcaccc	ttatggntcc	ctncctttng	gaactngcct	tttaatccnc	720
cngagggnt	tgctccttnt	ntttntgnnt	ggggaatna	aaagtn		766

<210> 539
 <211> 789
 <212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(789)

<223> n = A,T,C or G

<400> 539

accattggtg	gccaatgat	ttgatggtaa	gggagggatc	gttgacctcg	tctgttatgt	60
aaaggatgcg	tagggatggg	agggcgatga	ggactaggat	gatggcgggc	aggatagttc	120
agacggtttc	tatttcctga	gcgtctgaga	tgtagtatt	agttagtttt	gttgtgagt	180
ttaggaaaag	gcatacagga	ctaggaagca	gataaggaaa	atgattatga	gggcgtgatc	240
atgaaaggtg	ataagctctt	ctatgatagg	ggaagtagcg	tcttgtagac	ctacttgccg	300
tgcattgtgc	cccgctact	tgactttctt	ttntatttnt	tttattnttt	ttgactactt	360
agaattttca	caatttcta	aagattgttc	caagtctctc	atgtgcaagc	tttaaaggat	420
gactcttgcc	atztatgtac	ctcggnccgc	accacgctaa	gggcaaattc	agcacacttg	480
cggncgttct	aagtggatcc	nagctcggtc	caaccttgcg	tatcatggca	tactgggtccc	540
tngtgaaatg	tatcccttac	aatcncacac	atcnancccg	aanctaaann	taaanctggg	600
gccaaataata	ctactncata	atgctcnctn	ctgcenttca	ncnggaacnt	gtgcncctnt	660
tatnatggca	acncggaagn	gtggttggcc	ttcctctcta	aaacntgnng	gntngttgga	720
aggganctct	aggnnncggt	ccaattggan	ncgaaattnt	agctntntac	naaanatntt	780
tttttcncg						789

<210> 540

<211> 747

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(747)

<223> n = A,T,C or G

<400> 540

acttttaagg	gcataataag	ggttaacatt	ctaggcagta	taaacacacc	ccataatgca	60
agtaataggt	aatctagaga	tgtggacttt	attgctatat	gggaattaca	tttaaatttg	120
agggcatttt	atataaagaa	aaatacagac	ctataaagtt	tggcatattc	attaagttat	180
cttttaatat	ttttttctag	aaaacagggt	acatttgtat	ctacgataaa	aatttttata	240
cagaacctac	tgctcctca	tgaatcccat	caagaaaact	agtttctatt	gnattaagta	300
actcaaaaata	aattatcact	tcgaaaactt	gctttccaca	ctaaggtaag	tcagactaga	360
tgaacactcc	agaattttta	ctacagactg	ttttaagtta	gaagtgatgg	caattttata	420
attgagaata	tcctccctga	tgccctaact	ggccaaacca	aaatctaaga	aagcagtgc	480
ncctcttact	atnatgaact	tctgaatang	gtagggacct	cctggcntan	nnatgaaaan	540
ncctggccga	ccccctaggg	aatccncact	gggggcctnn	anggaccnan	tggccaantt	600
gnnannnggn	aangnnccctg	gnaatgtcen	caattcncna	atnccgncna	aagtaacnng	660
gcccnggggn	annnnnnangn	ngncnnccnn	nnngaannng	cccttnaann	ncccnggggg	720
ggngggntct	nnncnnnncc	nnngggg				747

<210> 541

<211> 773

<212> DNA

<213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(773)
 <223> n = A,T,C or G

<400> 541

cgagggtacca	tgaaatacat	atattttcata	aggttcagtt	acaaaatgga	ttgtttcaaa	60
tggcaatttc	ttacactaac	ctgattatga	aaaaaagaag	tctgtatcat	ctgcttccaa	120
gtctgttatg	tccaaatata	ttttaattat	gcatttat	tgctactttt	ataaatatta	180
gagatttcac	cttaaattat	ttttgtaact	agttctagaa	catgttttcc	aattattatt	240
tttctaattg	agacatataa	ttgacctatg	tttatgcata	tatgtttctt	acacagtga	300
acttttttta	aaaagaatag	taaagaaaat	gcggtagctc	tggctctcca	aggcaaagtc	360
aaaaaaaaaa	aaaaagcggg	ggggaatgcg	aggaacattt	tattacacct	cctgatttca	420
ctccttgagt	ttattttctc	ccttggttat	tggttaatgc	tagaaaactgn	attctaagag	480
agcatccttt	tcagggtgacn	tgataattgg	aagatttgat	ccttccgcga	cctgnccggc	540
ggcgcgtnaa	nggcnatcc	anccactggc	ggcgggttaa	nggatcnact	tggncacact	600
ggctaactgg	caacnggtcc	ngggngaaat	gnatccttaa	atccncactc	nacccgacct	660
aangaactgg	ggcaagggnc	accctatggg	gctcngcctt	cnngaantnn	cnnccttaan	720
aaccnggggn	gntgggnntct	nnnnnnnnnn	cnnttgngg	gnntaanaag	ann	773

<210> 542
 <211> 770
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(770)
 <223> n = A,T,C or G

<400> 542

cgagggtactt	tttttttttt	tttttttttt	tttttttttag	aattctgaat	tttatttagag	60
aatatatcta	aaatacaata	tttattaagt	tatgatatat	tgncatgaatg	gaaatatact	120
ctgnatcgca	actctaatta	taacaatttt	tacagataat	acttcattta	tatctctgna	180
attcaaaagt	cattaaatta	caacagaatt	catattttaag	ataactttgc	tataaatata	240
taataatttt	taaagttttt	ctttaatata	acatcttgaa	atcatgaaca	tttatttttt	300
ctgggttaca	ttcatagaat	catgactatt	ttacctgatt	tgccttaact	agctcaattt	360
atcttggcta	tggatttgca	ctcaccattc	tactttccta	tgtttaaaag	cacatttttag	420
tcacaattgn	gagtgtcat	caccctacat	gctgtgacaa	aggcaagggc	ctgcccgggc	480
ggccgtncaa	anggcgaatt	cncaactgg	cggcggtcca	agtggancga	ctcggaacca	540
ctngggaaca	tggcaactgg	tcccggggaa	atggaaccgt	acattcccca	natcagccga	600
ncttaggtaa	acngggggcn	aagggggcta	cncataatgg	nggtccnccc	ttcatngaac	660
cgngccctnn	tatnatgcac	cccggagggt	nnttngcctc	ctcntnnnnn	ntcngntgtg	720
gagggagtcc	ngggggggtnc	cangggggna	aaaantgccn	ngncccgng		770

<210> 543
 <211> 748
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(748)

<223> n = A,T,C or G

<400> 543

accgcgggat	gccccctcatt	tacataaata	ttatactagc	atttaccatc	tcactttctag	60
gaatactagt	atatcgctca	cacctcatat	cctccctact	atgcctagaa	ggaataatac	120
tatcgctggt	cattatagct	actctcataa	ccctcaacac	ccactccctc	ttagccaata	180
ttgtgectat	tgccatacta	gtctttgccc	ctgcgaagca	gcggtggggc	tagccctact	240
agtctcaatc	tccaacacat	atggcctaga	ctacgtacat	atgctaggcc	atatggtaac	300
tctatgttta	acatthttgag	gaactgccaa	actgttttcc	aaagtgacta	cactatthta	360
cattcccacc	ttgaagggtcc	aattttctga	cattctacca	acatgggtaa	tggctgcttt	420
ttatthtagca	accttaatgg	gtgtgaagag	atactcaatg	ggaatttgat	tgattcccta	480
angctaata	tggnthct	ttctggctga	ngccagagnt	atctnthtgg	gaaaattatt	540
naancttgnc	atthaacnng	cngatthtatn	tgatntanaa	tntthtattt	ggancnngcc	600
thtaagnaag	ntthaaaattn	ncaatnthtgg	ggctthcttt	tggccatgan	naannttaat	660
nttannanna	atthnnthn	annnggcnng	tnaannannn	nnnanaaana	annntthnna	720
anaannactt	ththnnnnna	cntggcgg				748

<210> 544

<211> 327

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(327)

<223> n = A,T,C or G

<400> 544

actthththth	ththththth	ththththth	ththththth	ththththth	ththththth	60
gggggtgcta	tagggtaaat	acgggcccta	ththcaaagat	ththtagggga	attaattctg	120
ggacgatggg	catgaaactg	tggtthtctc	cacagatthc	anagcattga	ccgtagtata	180
cccccggtcg	tgtagcggtg	aaagtggtht	ggtththaaacg	tccgggaatt	gcattctgtht	240
thtaagcctaa	tgthggggaca	gctcatgagt	gcaagacgtc	ththgatgta	attattatac	300
gaatgggggc	ththaatcggg	agthacct				327